

Supplementary Materials for: Integrated computational approach to the analysis of RNA-Seq data reveals new transcriptional regulators for psoriasis

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Running title: Transcriptional regulatory networks for psoriasis

Supplementary Table 1. Characteristics of psoriasis patients in the present study.

Nº	Patient Nº	Sex	Age	PASI
1	11	F	28	18
2	15	M	48	22
3	16	M	27	9
4	18	M	23	11
5	19	F	56	30
6	20	F	21	12
7	21	F	18	7
8	22	M	34	15
9	23	M	72	35
10	24	F	41	15
11	25	M	28	20
12	26	F	44	18
13	27	F	38	12
14	28	M	32	14

Supplementary Table 2. Top twenty upregulated genes according to the transcriptome analysis.

Gene name	Gene description	Fold Change	FDR
DEFB4B	defensin beta 4B	56.74	0.00
IL36A	interleukin 36, alpha	38.31	0.00
SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	36.69	2.67E-08
DEFB4A	defensin, beta 4A	33.30	0.00
SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	31.55	0.00
SERPINB11	serpin peptidase inhibitor, clade B (ovalbumin), member 11	28.58	0.00
TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	28.29	0.00
S100A8	S100 calcium binding protein A8	27.64	0.00
DEFB103B	defensin, beta 103B	25.16	0.00
S100A9	S100 calcium binding protein A9	23.82	0.00
CXCL1	chemokine (C-X-C motif) ligand 1	23.74	0.00
S100A12	S100 calcium binding protein A12	23.22	0.00
TMPRSS11D	transmembrane protease, serine 11D	22.69	0.00
S100A7A	S100 calcium binding protein A7A	21.59	0.00
PI3	peptidase inhibitor 3, skin-derived	21.39	0.00
SPRR2A	small proline-rich protein 2A	19.95	0.00
DEFB103A	defensin, beta 103A	19.23	1.72E-07

<i>NOS2</i>	nitric oxide synthase 2, inducible	18.53	2.09E-10
<i>OASL</i>	2'-5'-oligoadenylate synthetase-like	17.26	0.02
<i>AKR1B10</i>	aldo-keto reductase family 1, member B10 (aldose reductase)	17.01	0.00

Legend: Gene name - official gene symbol; Gene description – the description of gene name; Fold Change – fold change of gene expression in lesional versus non-lesional psoriatic skin; FDR – p-value, corrected for multiple comparisons. Zero values for paired p-value and FDR are used for the numbers less than 10^{-16} .

Supplementary Table 3. Top twenty downregulated genes according to the transcriptome analysis.

Gene name	Gene description	Fold Change	FDR
<i>GAL</i>	galanin prepropeptide	0.05	0.00
<i>FADS2</i>	fatty acid desaturase 2	0.05	4.28E-08
<i>PM20D1</i>	peptidase M20 domain containing 1	0.05	2E-04
<i>IGHEPI</i>	immunoglobulin heavy constant epsilon P1 pseudogene	0.05	3.24E-13
<i>HSD3B1</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	0.05	2E-03
<i>AWAT2</i>	acyl-CoA wax alcohol acyltransferase 2	0.06	0.00
<i>DGAT2L6</i>	diacylglycerol O-acyltransferase 2-like 6	0.06	0.03
<i>snoU13</i>	small nucleolar RNA U13	0.06	1.72E-08
<i>ELOVL3</i>	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	0.06	4E-03
<i>THRSP</i>	thyroid hormone responsive (SPOT14 homolog, rat)	0.07	4.16E-05
<i>RP4-539M6</i>	novel lincRNA	0.07	2.8E-03
<i>AWAT1</i>	acyl-CoA wax alcohol acyltransferase 1	0.07	0.02
<i>RP11-546K22.1</i>	novel lincRNA	0.08	1.54E-10
<i>HAO2</i>	hydroxyacid oxidase 2 (long chain)	0.08	4E-03
<i>PNPLA5</i>	patatin-like phospholipase domain containing 5	0.08	5.45E-05
<i>RP11-247A12.1</i>	novel lincRNA	0.09	1.44E-09
<i>IGHE</i>	immunoglobulin heavy constant epsilon	0.09	2.54E-07
<i>CRAT</i>	carnitine acetyltransferase	0.10	2.8E-03
<i>HSD3BP2</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta, pseudogene 2	0.10	9.40E-06
<i>MOGAT2</i>	monoacylglycerol O-acyltransferase 2	0.11	1.29E-10

Legend: Gene name - official gene symbol; Gene description – the description of gene name; Fold Change – fold change of gene expression in lesional versus non-lesional psoriatic skin; FDR – p-value, corrected for multiple comparisons. Zero values for paired p-value and FDR are used for the numbers less than 10^{-16} .

Supplementary Table 4. Gene Ontology pathway enrichment according to the transcriptome analysis.

GO pathway ID	Number of genes in the cascade	p-value
Activated pathways		
hsa04060:Cytokine-cytokine receptor interaction	53	1,20E-14
hsa04062:Chemokine signaling pathway	39	3,10E-11
hsa04630:Jak-STAT signaling pathway	23	1.72E-05
hsa04650:Natural killer cell mediated cytotoxicity	26	4,39E-07
hsa04621:NOD-like receptor signaling pathway	17	7,05E-07
hsa04640:Hematopoietic cell lineage	17	6,31E-05

hsa05332:Graft-versus-host disease	11	9,63E-05
hsa04612:Antigen processing and presentation	16	1,51E-04
hsa04514:Cell adhesion molecules (CAMs)	20	4,67E-04
hsa04623:Cytosolic DNA-sensing pathway	11	5.11E-04
Inhibited pathways		
hsa03320:PPAR signaling pathway	12	1,12E-05
hsa01040:Biosynthesis of unsaturated fatty acids	5	0.0015
hsa00140:Steroid hormone biosynthesis	6	0.007
hsa00910:Nitrogen metabolism	2	0.020
hsa04270:Vascular smooth muscle contraction	7	0.046
hsa04020: Calcium signaling pathway	9	0.050
hsa00640:Propanoate metabolism	4	0.051

Legend: GO pathway ID - the ID of gene ontologies signaling pathway according to DAVID database; **Number of genes in the cascade** – the number of genes in the DEG list present in this cascade; p-value ≤ 0.05 .

Mapping of DEGs to psoriasis-associated loci

We analyzed the distribution of DEGs between chromosomal locations (cytobands) (Supplementary Table 5). Since psoriasis is a systemic disorder that involves different tissues (skin, the underlying blood vessels, the immune system and the adipose tissue) (1-3), closely located DEGs can be co-expressed during development of psoriatic skin lesions. Recent genome-wide association studies (GWASs) and meta-analysis of GWAS of psoriasis in European individuals have identified a total of 36 psoriasis susceptibility loci (PSORS) at a genome-wide level of significance (4). In order to find the association between PSORS and psoriatic histopathology alterations, we analyzed the distribution of the 20 most upregulated genes that has revealed three groups of genes located in the same chromosomal location. Close proximity of these genes indicates that these gene clusters could be orchestrated together in the affected skin. Taking into account that these genes were also united by common functions, we marked these proposed clusters as "EDC", "DEF" and "SER". The orchestrated expression changes of genes located in close proximity to each other are possibly mediated by the activity of common transcription factors (TF).

Supplementary Table 5. Clustering of top DEG genes by location

Gene symbol	Cytoband	Cluster	Gene symbol	Cytoband	Cluster
Up-regulated genes			Down-regulated genes		
DEFB4B	8p23.1	DEF	GAL	11q13.2	
IL36A	2q13		FADS2	11q12-q13.1	
SERPINB4	18q21.3	SER	PM20D1	1q32.1	
DEFB4A	8p23.1-p22	DEF	IGHEP1	14q32.33	C2
SERPINB3	18q21.3	SER	HSD3B1	1p13.1	C1 (PSORS7)
SERPINB11	18q21.3	SER	AWAT2	Xq13.1	
TCN1	11q11-q12		DGAT2L6	Xq13.1	

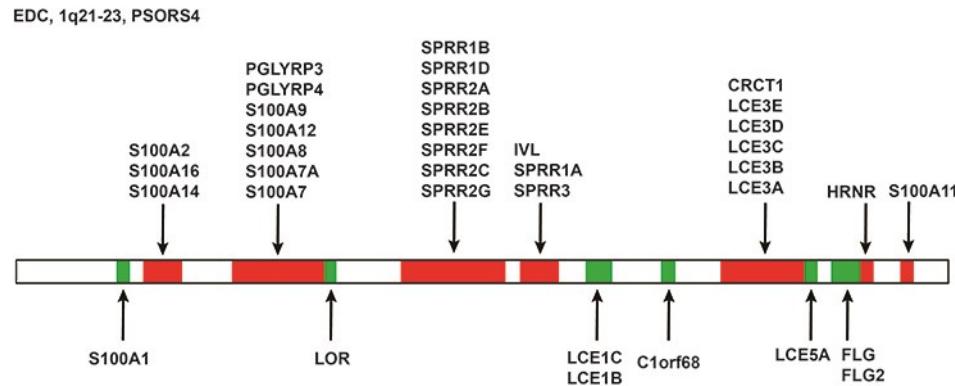
S100A8	1q21	EDC	<i>snoU13</i>	1p36.21	
DEFB103B	8p23	DEF	<i>ELOVL3</i>	10q24.32	
S100A9	1q21	EDC	<i>THRSP</i>	11q14.1	C3
CXCL1	4q21		<i>RP4-539M6</i>	22q12.2	
S100A12	1q21	EDC	<i>AWAT1</i>	Xq13.1	
TMPRSS11D	4q13.2		<i>RP11-546K22.1</i>	8q11.3	
S100A7A	1q21	EDC	<i>HAO2</i>	1p13.3-p13.1	C1 (PSORS7)
PI3	20q12-q13		<i>PNPLA5</i>	22q13.31	
SPRR2A	1q21-q22	EDC	<i>RP11-247A12.1</i>	9q34.11	
DEFB103A	8p23	DEF	<i>IGHE</i>	14q32.33	C2
NOS2	17q11.2-q13		<i>CRAT</i>	9q34.1	
OASL	12q24.31		<i>HSD3BP2</i>	1p13.1	C1 (PSORS7)
AKR1B10	7q33		<i>MOGAT2</i>	11q13.5	C3

Legend: **Gene symbol** – official gene symbol according to NCBI gene database; **Cytoband** - the chromosomal localisation of a gene; **Cluster** – the putative orchestrated cluster of genes, a group of genes located in the same chromosomal location and expressed coordinately.

EDC (epidermal differentiation complex, the cytoband **1q21**) is a 2-Mb locus, also known as **PSORS4** (psoriasis susceptibility locus 4). It contains genes playing crucial roles in differentiation of epidermal keratinocytes, a dominant type of skin cells. Activation of keratinocytes by immunocytes not only impairs keratinocyte differentiation, but also leads to their enhanced proliferation and further production of chemo-attractive molecules that eventually lead to the development of psoriatic plaques. EDC is comprised of genes encoding structural and regulatory proteins important for the development of stratum corneum, the outermost layer of epidermis accounting for the barrier functions of skin.

Among the DEGs that belong to the epidermal differentiation complex were genes encoding EF-hand calcium-binding proteins from the S100A family, genes encoding the small proline rich proteins (SPRRs), genes of late cornified envelope (LCE) proteins, as well as genes encoding the S100-fused type proteins (SFTPs) – for example, *FLG* (Supplementary Figure 1). The main functions of these proteins in adult epidermis are cornified envelope reinforcement and recovery of the epidermal barrier during wound healing as well as antimicrobial activity (S100 proteins). Concordant expression of the EDC genes during embryonic skin development and adult epidermal differentiation suggests a genomic mechanism and common regulatory elements to control their transcription (5). Clustering of the EDC genes, their structural relationship and functional interdependence of the encoded proteins confirmed that certain EDC may act together as a group. Moreover, the expression of these genes can change coordinately, in certain physiological and pathological conditions (6). Particularly, Jackson et al. discovered that a stimulation of cultured epidermal keratinocytes with either UV light or calcium results in modification of LCE gene expression (7). Applying the UV-light stimulated LCE1 and LCE2 (2A, 2B, 2C and 2D) genes that are abundant in healthy skin LCE3E expressed in the skin at a very low level. Treatment with calcium specifically induced LCE2

genes (2A, 2B, 2C and 2D). A different change occurs in psoriatic skin. Bergboer et al. reported that lesional skin exhibits an altered LCE expression profile (8). According to their data, LCE1 and LCE2 expression is suppressed. The LCE3 genes are upregulated compared to the unaffected skin areas. In our study, we report the correlated gene expression in three groups of EDC genes, namely LCE, SPRR and S100. We showed (Supplementary Table 1) that both LCE1D and LCE1E are upregulated in lesional skin.

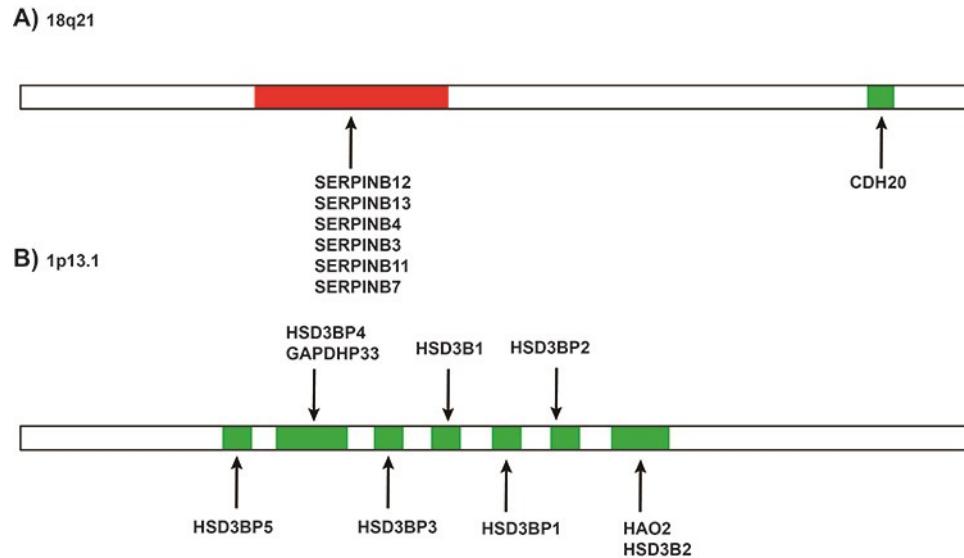


Supplementary Figure 1. Schematic representation of EDC, epidermal differentiation complex. Up- and down-regulated GEGs are marked in red and green color, respectively.

DEF is a cluster of defensins (the cytoband **8p23.1**). Proteins encoded by these genes contribute to antimicrobial defense. Different defensins act as chemo-attractants for T-cells, dendritic cells, monocytes, macrophages, neutrophils, and activate Th1-mediated response. In addition, *HBD2-4* can stimulate proliferation and migration of keratinocytes and prepare them for enhanced production of pro-inflammatory cytokines and chemokines. IL-6, IL-10, MCP-1, MIP-3 α , RANTES, IP-10, and *HBD3-4* can induce pDC production of IFNs and degranulation of mast cells (9). It has been shown that copy number variation of beta-defensin genes is a risk factor for increased susceptibility to psoriasis (10). In our RNA-Seq experiment all the defensin genes mentioned above showed elevated expression levels (DEFB103A FC=19,23; DEFB103B FC=25,16; DEFB4A FC=33,30; DEFB4B FC=56,73).

SER is a cluster of serpin B genes (Supplementary Figure 2A). The SER cluster composed of six SERPINB genes, namely SERPINB12 (upregulated, FC=1.80), SERPINB13 (upregulated, FC=2.60), SERPINB4 (upregulated, FC=8.40), SERPINB3 (upregulated, FC=8.20), SERPINB11 (upregulated, FC=9.08), SERPINB7 (upregulated, FC=1.86) that follow each other on chromosome 18 in the strict order. Although the role of SERPINB is yet to be determined, there is strong association between SERPINB genes with oral squamous carcinoma (11). The proteins encoded by these genes play a significant role in maintenance of proteolytic balance within epidermis. Interestingly, the authors (11) suggest that seven SERPINB i.e. six genes that we report as well as the SERPINB2 genes are downregulated as a group. This suggests existence of common regulatory elements in the genome allowing co-regulation of gene expression. However, our data indicate upregulation of SERPINBs in lesional skin. We propose that correlated upregulation of SERPINBs genes can contribute to tissue remodeling within the psoriatic

plaques, including modification of extracellular matrix due to a balance shift between proteases and their inhibitors. What is more, serpins play an important role in modulating proliferation/apoptosis rates by contrasting cytochrome c release from the mitochondria and by antichemotactic effect for NK cells. Mechanisms involved in apoptosis induction and regulation play a key role in the balance between cell proliferation and death. Disturbance of this equilibrium may contribute to the development of autoimmune diseases, as defective apoptosis of immune cells leads to deregulated autoreactive cell proliferation (12).



Supplementary Figure 2. Schematic representation of gene clusters "SER" and C1 (see explanations in the text). Up- and downregulated GEGs are marked in red and green color, respectively.

In addition, several gene clusters, namely **C1** (the cytoband **1p13.1**), **C2** (the cytoband **14q32.33**), and **C3** (the cytoband **11q13.5**) were identified among the downregulated genes (Supplementary Figure 2B). However, the detailed mapping of regions where these clusters could be located did not confirm an existence of the clusters C2 and C3, but we were able to map cluster C1, which was composed of 9 closely located from each other downregulated genes. This locus is strongly associated with plasma low-density lipoprotein cholesterol (LDLC) and very low-density lipoprotein (VLDL) levels and the elevated risk of myocardial infarction (13). It is mostly composed of HSD3B genes, namely HSD3B1-2, HSD3BP1-5. This cluster also includes the HAO2 and GAPDHP33. HSD3BP1-5 and GAPDHP33 are considered as pseudogenes because they contain internal stop codons within the open reading frames (8). At the same time, the specific mRNAs that belong to HASDBPs are occasionally found in some tissues.

3β -hydroxysteroid dehydrogenase/isomerase (3β -HSD) converts 3-hydroxy $\Delta 5$ precursors to 3-keto $\Delta 4$ products and initiates the biosynthesis of mineralocorticoid, glucocorticoid, and sex hormones (14, 15). HSD3B1 is expressed in placenta and skin. In contrast, HSDB2 is a principal enzyme in adrenals and gonads (16). Low HSD3B2 activity caused by mutations is linked to several diseases, such as adrenal hyperplasia and male

pseudohermaphroditism (17). Although no particular association of either HSD3B1 or HSD3B2 downregulation with psoriasis has been found, some studies link HSD3B1 deficiency with hyperplasia in several tissues, other than epidermis (18, 19). In this study, we report that both HSD3B1 and HSD3B1 are downregulated in psoriatic plaques (0.055 and 0.28, respectively). Moreover, the genes that comprise the C1 cluster can be regulated as a group and contribute to epidermal hyperplasia.

Supplementary Table 6. Transcriptional regulators of DEG, as identified by MetaCore Interactome analysis.

Object name	Actual (A)	R	Expected (E)	Ratio (R)	Z-score	p-value
STAT1	76	337	15.10	5.03	16.14	3.17E-32
NF-kB	65	311	13.93	4.67	14.08	1.00E-25
IRF8	57	250	11.20	5.09	14.07	1.05E-24
p50	79	441	19.76	4.00	13.75	2.47E-26
T-bet	22	49	2.20	10.02	13.69	2.75E-17
RelA	110	778	34.85	3.16	13.22	4.54E-27
p50/p65	44	176	7.88	5.58	13.20	4.67E-21
c-Rel	48	211	9.45	5.08	12.88	5.77E-21
IRF1	46	198	8.87	5.19	12.80	1.52E-20
PU.1	68	380	17.02	3.99	12.73	8.63E-23
AP-1	57	290	12.99	4.39	12.56	2.46E-21
PPARγ	51	266	11.92	4.28	11.64	9.73E-19
STAT6	39	175	7.84	4.97	11.42	5.79E-17
STAT3	80	557	24.95	3.21	11.39	2.39E-20
C/EBPb	80	592	26.52	3.02	10.74	1.01E-18
ISGF3	10	18	0.81	12.40	10.48	9.89E-10
C/EBPa	56	361	16.17	3.46	10.20	4.3E-16
SP1	149	1553	69.57	2.14	10.04	5.75E-19
LXRa	24	95	4.26	5.64	9.81	3.15E-12
c-Jun	89	768	34.41	2.59	9.66	2.1E-16
STAT5A	25	105	4.70	5.31	9.59	4.67E-12
PPARγ/RXRa	25	105	4.70	5.31	9.59	4.67E-12
STAT5B	19	68	3.05	6.24	9.36	8.52E-11
IRF7	14	41	1.84	7.62	9.19	1.38E-09
STAT2	19	71	3.18	5.97	9.09	1.94E-10
c-Fos	42	271	12.14	3.46	8.81	2.14E-12
p50/p50	18	68	3.05	5.91	8.78	7.06E-10
NR3C4	96	930	41.66	2.30	8.77	2.13E-14
RelB	34	198	8.87	3.83	8.67	1.5E-11
p105	15	53	2.37	6.32	8.39	6.78E-09
p65/p65	10	26	1.16	8.59	8.38	8.64E-08
GCRa	110	1177	52.73	2.09	8.25	1.99E-13
C/EBPe	10	27	1.21	8.27	8.18	1.32E-07
IRF9	9	23	1.03	8.73	8.04	3.26E-07
NKRF	3	3	0.13	22.32	8.00	8.97E-05
E2F1/DP1	5	8	0.36	13.95	7.93	8.95E-06
STAT5	20	94	4.21	4.75	7.89	5.19E-09
JunD	30	183	8.20	3.66	7.82	7.48E-10
ETS1	48	378	16.93	2.83	7.78	8.76E-11
p53	98	1055	47.26	2.07	7.70	6.37E-12

Oct-1	28	169	7.57	3.70	7.62	2.14E-09
GRHL2	12	42	1.88	6.38	7.55	1.96E-07
STAT4	10	31	1.39	7.20	7.48	5.88E-07
Bcl-6	23	128	5.73	4.01	7.39	1.18E-08
JunB	22	120	5.38	4.09	7.35	1.67E-08
ETS	14	57	2.55	5.48	7.34	1.54E-07
ELF4	6	13	0.58	10.30	7.27	1.04E-05
ESR1 (nuclear)	105	1208	54.12	1.94	7.24	5.67E-11
CAR/RXRα	8	22	0.99	8.12	7.23	2.89E-06
VDR	30	202	9.05	3.32	7.15	8.2E-09
EGR3	7	18	0.81	8.68	7.06	7.33E-06
NF-AT1(NFATC2)	17	87	3.90	4.36	6.80	2.68E-07
IRF2	15	71	3.18	4.72	6.79	4.65E-07
NF-kB2 (p52)	19	105	4.70	4.04	6.76	1.93E-07
C/EBPδ	24	154	6.90	3.48	6.68	9.88E-08
Fra-2	14	66	2.96	4.73	6.58	1.06E-06
CREB5	2	2	0.09	22.32	6.53	0.002005
IRF3	12	53	2.37	5.05	6.40	3E-06
POLR2A	7	21	0.94	7.44	6.39	2.38E-05
HNF4α	48	451	20.20	2.38	6.38	3.01E-08
RXRA	23	152	6.81	3.38	6.37	3.13E-07
SREBP1 (nuclear)	22	144	6.45	3.41	6.28	4.74E-07
VDR/RXRα	15	80	3.58	4.19	6.18	2.31E-06
RBP-Jκ(CBF1)	19	117	5.24	3.62	6.16	1.1E-06
HNF1α	31	251	11.24	2.76	6.06	3.46E-07
PXR/RXRα	7	23	1.03	6.79	6.02	4.64E-05
c-Jun/c-Fos	14	74	3.32	4.22	6.01	4.47E-06
Tip60	3	5	0.22	13.39	6.00	0.000838
LITAF	3	5	0.22	13.39	6.00	0.000838
E2F3/DP1	3	5	0.22	13.39	6.00	0.000838
KLF6	10	43	1.93	5.19	5.96	1.56E-05
KLF13	4	9	0.40	9.92	5.80	0.000421
ATF-3	16	97	4.35	3.68	5.73	6.17E-06
GFI-1	9	38	1.70	5.29	5.73	3.55E-05
TBP	17	108	4.84	3.51	5.67	6.15E-06
HMGI/Y	11	54	2.42	4.55	5.65	2.26E-05
HIF1A	55	601	26.92	2.04	5.60	4.85E-07
RXR	7	26	1.16	6.01	5.53	0.000111
CREM (repressors)	9	40	1.79	5.02	5.51	5.49E-05
EGR2 (Krox20)	13	73	3.27	3.98	5.51	1.94E-05
NCOA2 (GRIP1/TIF2)	4	10	0.45	8.93	5.43	0.000677
ASH2	5	15	0.67	7.44	5.40	0.000369
ZNF263	3	6	0.27	11.16	5.39	0.00162
EGFR	3	6	0.27	11.16	5.39	0.00162
PURB	3	6	0.27	11.16	5.39	0.00162
GATA-3	56	632	28.31	1.98	5.39	1.06E-06
PAX5	19	137	6.14	3.10	5.33	1.19E-05
ETS2	17	117	5.24	3.24	5.27	1.83E-05
p73	20	150	6.72	2.98	5.26	1.29E-05

LXRβ/RXRα	7	28	1.25	5.58	5.25	0.000184
LXRα/RXRα	9	43	1.93	4.67	5.22	0.0001
FXR	18	129	5.78	3.11	5.21	1.85E-05
NF45 (ILF2)	2	3	0.13	14.88	5.21	0.005837
SOX13	2	3	0.13	14.88	5.21	0.005837
NFYB	17	119	5.33	3.19	5.18	2.29E-05
ERM	5	16	0.72	6.98	5.18	0.000517
SP3	45	486	21.77	2.07	5.14	3.85E-06
E2F4	33	317	14.20	2.32	5.13	6.75E-06
PPARα	22	177	7.93	2.77	5.13	1.52E-05
Nkx6.1	4	11	0.49	8.12	5.11	0.001027
Zac1	4	11	0.49	8.12	5.11	0.001027
RUNX3	10	53	2.37	4.21	5.07	0.000105
FOXO3A	22	179	8.02	2.74	5.07	1.81E-05
Fra-1	12	71	3.18	3.77	5.07	6.85E-05
p63	40	419	18.77	2.13	5.05	6.35E-06
EBF	17	123	5.51	3.09	5.02	3.54E-05
AML1 (RUNX1)	26	232	10.39	2.50	4.97	1.74E-05
KLF5	10	55	2.46	4.06	4.92	0.000146
JunD/c-Fos	3	7	0.31	9.57	4.91	0.002741
NFYA	17	126	5.64	3.01	4.90	4.84E-05
PLZF/RARα	12	74	3.32	3.62	4.89	0.000104
c-Myb	20	161	7.21	2.77	4.89	3.67E-05
HIF-1	11	65	2.91	3.78	4.86	0.000135
ATF-2	20	162	7.26	2.76	4.85	4.01E-05
C/EBP	10	56	2.51	3.99	4.84	0.00017
IRF5	8	39	1.75	4.58	4.84	0.000282
p65/c-Rel	4	12	0.54	7.44	4.83	0.001486
EGR1	40	434	19.44	2.06	4.81	1.46E-05
SRF	37	401	17.96	2.06	4.63	2.93E-05
AP-2B	6	26	1.16	5.15	4.59	0.000849
DEC1 (Stra13)	11	70	3.14	3.51	4.55	0.000266
IRF4	39	438	19.62	1.99	4.51	4E-05
PURα	5	20	0.90	5.58	4.44	0.001579
ZHX2	2	4	0.18	11.16	4.40	0.011327
RBCK1	2	4	0.18	11.16	4.40	0.011327
E2F4/DP1	2	4	0.18	11.16	4.40	0.011327
HOXB8	2	4	0.18	11.16	4.40	0.011327
RFX5	4	14	0.63	6.38	4.36	0.002796
MafK	4	14	0.63	6.38	4.36	0.002796
BACH2	6	28	1.25	4.78	4.34	0.001287
NUR77	8	45	2.02	3.97	4.32	0.000779
NF-Y	22	208	9.32	2.36	4.27	0.000175
HNF3α	20	182	8.15	2.45	4.26	0.000203
PPARα/RXRα	13	97	4.35	2.99	4.26	0.000388
FosB	9	56	2.51	3.59	4.20	0.0008
KLF8	3	9	0.40	7.44	4.18	0.006148
TCF7L2 (TCF4)	31	339	15.19	2.04	4.18	0.000148
ATF-4	12	88	3.94	3.04	4.16	0.000547
DLX4 (BP1)	4	15	0.67	5.95	4.15	0.003679

FOXP3	23	227	10.17	2.26	4.13	0.000238
ELF3	6	30	1.34	4.46	4.11	0.001879
FKHR	22	215	9.63	2.28	4.09	0.00028
NRF2	18	162	7.26	2.48	4.09	0.000362
BACH1	7	39	1.75	4.01	4.07	0.001555
E2F5	5	23	1.03	4.85	4.00	0.003066
E2F8	5	23	1.03	4.85	4.00	0.003066
BATF	4	16	0.72	5.58	3.97	0.004733
E2F2	14	116	5.20	2.69	3.96	0.000695
C/EBPz	12	93	4.17	2.88	3.93	0.000905
IRF6	3	10	0.45	6.70	3.90	0.008493
CREB3	3	10	0.45	6.70	3.90	0.008493
LXRb	7	41	1.84	3.81	3.90	0.002103
RARα	15	130	5.82	2.58	3.90	733
BLIMP1	11	83	3.72	2.96	3.87	1.17E-03
LDB1	2	5	0.22	8.93	3.84	0.02
TLE3	2	5	0.22	8.93	3.84	0.02
ADNP	2	5	0.22	8.93	3.84	0.02
SMAD2	15	134	6.00	2.50	3.77	1.01E-03
ELF5	5	25	1.12	4.46	3.75	4.50E-03
CBFβ	7	43	1.93	3.63	3.74	2.79 E-04
KLF2	6	34	1.52	3.94	3.71	3.66E-03
Lef-1	15	136	6.09	2.46	3.70	1.17E-03
FOXP2	20	204	9.14	2.19	3.69	8.92E-04
ELF1	11	87	3.90	2.82	3.69	1.73E-03
FOXM1	12	99	4.44	2.71	3.68	1.57E-03
NF-E2	8	54	2.42	3.31	3.67	2.64E-03
E2F3	16	150	6.72	2.38	3.67	1.1E-03
USF1	21	219	9.81	2.14	3.67	8.95E-04
PXR	7	44	1.97	3.55	3.67	3.19E-03
ERR2	10	76	3.40	2.94	3.66	2.04E-03
AP-2A	24	263	11.78	2.04	3.66	8.12E-04
HFH3	3	11	0.49	6.09	3.65	0.01
ESR2	15	138	6.18	2.43	3.64	1.36E-03
RORγ	5	26	1.16	4.29	3.64	5.36E-03
Ikaros	9	66	2.96	3.04	3.60	2.62E-03
GLI-2	7	45	2.02	3.47	3.59	3.64E-03
ERR1	19	194	8.69	2.19	3.59	1.20E-03
RORα	10	78	3.49	2.86	3.57	2.48E-03
AHR	22	239	10.71	2.05	3.55	1.17E-03
Oct-2	6	36	1.61	3.72	3.54	4.91E-03
HNF3g	4	19	0.85	4.70	3.49	9.06E-03
E4BP4	8	57	2.55	3.13	3.49	3.72E-03
E2A	12	104	4.66	2.58	3.49	2.39E-03
RUNX2	16	157	7.03	2.27	3.47	1.88E-03
c-Jun/Fra-1	3	12	0.54	5.58	3.44	0.01
MBD1	3	12	0.54	5.58	3.44	0.01
β-catenin	3	12	0.54	5.58	3.44	0.01
ZNF202	4	20	0.90	4.46	3.36	0.01
TCF7 (TCF1)	5	29	1.30	3.85	3.32	8.67E-03

	MafB	5	29	1.30	3.85	3.32	8.67E-03
AP-4		8	60	2.69	2.98	3.32	5.13E-03
TRβ1		12	109	4.88	2.46	3.30	3.54E-03
E2F1		53	771	34.54	1.53	3.26	1.42E-03
NeuroD/E47		3	13	0.58	5.15	3.24	0.02
NFIB		5	30	1.34	3.72	3.23	0.01
p50/c-Rel		4	21	0.94	4.25	3.23	0.01
PEA3		9	74	3.32	2.71	3.20	0.01
KLF4		23	272	12.19	1.89	3.19	2.78E-03
CREM (activators)		10	87	3.90	2.57	3.17	5.50E-03
TAL1		17	183	8.20	2.07	3.16	3.67 E-03
CLOCK		9	75	3.36	2.68	3.15	0.01
KLF15		5	31	1.39	3.60	3.14	0.01
TITF1		10	88	3.94	2.54	3.13	0.01
MEF2C		8	64	2.87	2.79	3.11	0.01
NRF1		13	130	5.82	2.23	3.05	0.01
BMAL1		11	104	4.66	2.36	3.01	0.01
LRH1		11	104	4.66	2.36	3.01	0.01
TRα		10	91	4.08	2.45	3.01	0.01
PML/RARα		6	43	1.93	3.11	3.01	0.01
USF1/USF2		6	43	1.93	3.11	3.01	0.01
CAR		4	23	1.03	3.88	2.99	0.02
KLF11 (TIEG2)		4	23	1.03	3.88	2.99	0.02
SREBP1		5	33	1.48	3.38	2.97	0.02
ZNF145		5	33	1.48	3.38	2.97	0.02
SOX9		11	106	4.75	2.32	2.94	7.96E-03
GATA-1		28	367	16.44	1.70	2.94	4.53E-03
b-Myb		10	93	4.17	2.40	2.93	8.744E-03
PAX8		10	93	4.17	2.40	2.93	0.008744
USF2		13	134	6.00	2.17	2.93	0.007242
SREBP2 (nuclear)		8	68	3.05	2.63	2.91	0.010835
ZNF42 (MZF1)		6	45	2.02	2.98	2.87	0.014608
HNF3β		21	260	11.65	1.80	2.82	0.006923
AML1/ETO		9	83	3.72	2.42	2.81	0.011895
FoxL2		7	58	2.60	2.69	2.80	0.014609
AP-2C		12	125	5.60	2.14	2.77	0.010445
DBP		29	396	17.74	1.63	2.76	0.006857
NFIC		6	47	2.11	2.85	2.75	0.017865
POU3F2 (BRN2)		10	98	4.39	2.28	2.74	0.012427
SNAIL1		8	72	3.23	2.48	2.72	0.01502
PR (nuclear)		19	238	10.66	1.78	2.62	0.011085
HSF1		21	273	12.23	1.72	2.58	0.011684
LHX2		27	382	17.11	1.58	2.46	0.013644
ZNF143		18	1013	45.38	0.40	-4.24	1.58E-06

Legend: Object name – the name of transcriptional factor; **Actual (A)** - number of targets of this transcriptional factor in the DEG list; **R** - number of targets of this transcriptional factor in the complete database; **Expected** - the number of objects of this class that would be expected to occur in the dataset purely by chance; **Ratio** - connectivity ratio (Actual/Expected); **Z-score** - enrichment score of number of targets of this TF in the DEG list ((Actual-Expected)/Standard Deviation)

Expected)/sqrt(variance)); **p-value** - probability to have the given or higher (lower for negative z-score) value of Actual by chance under null hypothesis of no over- or under-connectivity.

Supplementary Table 7. Novel putative transcriptional regulators of DEGs.

Object name	Actual	R	Expected	Ratio	Z-score	p-value
NKRF	3	3	0.13	22.32	8.00	8.97E-05
ETS1	48	378	16.93	2.83	7.78	8.76E-11
ELF4	6	13	0.58	10.30	7.27	1.04E-05
ESR1 (nuclear)	105	1208	54.12	1.94	7.24	5.67E-11
CAR/RXR-alpha	8	22	0.99	8.12	7.23	2.89E-06
EGR3	7	18	0.81	8.68	7.06	7.33E-06
HNF4-a	48	451	20.20	2.38	6.38	3.01E-08
SREBP1 (nuclear)	22	144	6.45	3.41	6.28	4.74E-07
RBP-Jk (CBF1)	19	117	5.24	3.62	6.16	1.10E-06
HMGI/Y	11	54	2.42	4.55	5.65	2.26E-05
EGR2 (Krox20)	13	73	3.27	3.98	5.51	1.94E-05
ASH2	5	15	0.67	7.44	5.40	3.69E-04
ZNF263	3	6	0.27	11.16	5.39	1.62E-03
PURB	3	6	0.27	11.16	5.39	1.62E-03
NF45 (ILF2)	2	3	0.13	14.88	5.21	5.84E-03
NFYB	17	119	5.33	3.19	5.18	2.29E-05
Nkx6.1	4	11	0.49	8.12	5.11	1.03E-03
FOXO3A	22	179	8.02	2.74	5.07	1.81E-05
NFYA	17	126	5.64	3.01	4.90	4.84E-05
PLZF/RARα fusion protein	12	74	3.32	3.62	4.89	1.04E-04
PUR-alpha	5	20	0.90	5.58	4.44	1.58E-03
RBCK1	2	4	0.18	11.16	4.40	1.13E-02
FKHR	22	215	9.63	2.28	4.09	2.80E-04
E2F5	5	23	1.03	4.85	4.00	3.07E-03
TLE3	2	5	0.22	8.93	3.84	1.83E-02
ELF5	5	25	1.12	4.46	3.75	4.50E-03
CBF beta	7	43	1.93	3.63	3.74	2.79E-03
FOXP2	20	204	9.14	2.19	3.69	8.92E-04
USF1	21	219	9.81	2.14	3.67	8.95E-04
ERR2	10	76	3.40	2.94	3.66	2.04E-03
FOXA1	3	11	0.49	6.09	3.65	1.13E-02
IKZF1	9	66	2.96	3.04	3.60	2.62E-03
ERR1	19	194	8.69	2.19	3.59	1.20E-03

MBD1	3	12	0.54	5.58	3.44	1.46E-02
TFAP4	8	60	2.69	2.98	3.32	5.13E-03
NeuroD/E47	3	13	0.58	5.15	3.24	1.83E-02
SREBP1 precursor	5	33	1.48	3.38	2.97	1.50E-02
FOXA2	21	260	11.65	1.80	2.82	6.92E-03

Legend: **Object name** – the name of transcriptional factor; **Actual** - number of targets of this transcriptional factor in the DEG list; **R** - number of targets of this transcriptional factor in the complete database; **Expected** - the number of objects of this class that would be expected to occur in the dataset purely by chance; **Ratio** - connectivity ratio (Actual/Expected); **Z-score** - enrichment score of number of targets of this TF in the DEG list ((Actual-Expected)/sqrt(variance)); **p-value** - probability to have the given or higher (lower for negative z-score) value of Actual by chance under null hypothesis of no over- or under-connectivity.

Supplementary Table 8. Motifs identified with cisExpress using expression data and promoter sequences.

From...to	Motif	Z-score	From...to	Motif	Z-score
-970...-950	gcatc	-4,03827	-20...0	tgacg	4,93224
-890...-870	tatgt	5,0581	-20...0	ceggaa	5,86833
-770...-750	ctcgg	4,64115	-10...10	aatgg	4,06469
-720...-700	ccagg	-4,13045	-10...10	cagac	-4,87773
-720...-700	cgaca	-4,3816	-10...10	cagca	-4,00185
-720...-700	gtegt	4,77533	-10...10	gccat	5,37224
-690...-670	ccgat	4,36935	-10...10	ggegg	4,18635
-640...-620	gctta	4,20631	-10...10	tcacg	4,33167
-620...-600	cgaaa	4,00891	-10...10	cac[ct]c	-5,7075
-550...-530	cgatc	4,31686	0...20	aagat	5,56491
-480...-460	gaaca	4,24056	0...20	cacag	-4,21346
-470...-450	acgga	5,0913	0...20	gatggc	5,31152
-460...-440	ctacc	4,34911	0...20	tggcgg	4,32401
-450...-430	gcaca	-4,12148	10...30	agetc	-4,03147
-420...-400	cgccg	4,17182	10...30	aagatg	7,03792
-380...-360	gttca	4,18928	10...30	gatggc	4,62403
-380...-360	tgtat	-4,02851	10...30	tggcgg	5,63698
-370...-350	acgcc	4,46565	20...40	atggeg[gt]c	4,52363
-340...-320	aggga	-4,5553	30...50	cacag	-4,46581
-310...-290	ctggg	-4,01667	30...50	ctget	-4,2837
-310...-290	tgggt	-4,45678	40...60	acaat	4,0285
-280...-260	acgat	4,92803	40...60	ctget	-4,11016
-270...-250	ttct	-4,06828	50...70	agggg	4,37231
-260...-240	tactc	5,09423	60...80	atacg	4,80276
-240...-220	cggtt	4,10662	70...90	atacg	4,75889
-230...-210	agcga	4,09665	70...90	ttgcg	4,21913
-220...-200	accgg	4,00058	80...100	aacga	4,30182
-210...-190	cagga	-4,36467	80...100	ccgtt	4,05443

-180...-160	cgeaa	4,49834	200...220	tccgc	4,91439
-170...-150	cctgg	-4,70938	230...250	ggcgg	4,11269
-140...-120	tccgt	4,24841	230...250	tcttg	4,04838
-130...-110	ctaag	4,05098	250...270	gcttc	4,02731
-100...-80	cggaa	4,47074	300...320	ccgtt	5,42565
-100...-80	tecg	4,29905	330...350	accca	-4,18038
-100...-80	tgtca	-4,03306	340...360	cgctc	4,07522
-90...-70	agact	4,61066	350...370	cggtt	4,6605
-90...-70	cgaga	4,14169	360...380	acgta	4,18762
-70...-50	gaec	4,35674	360...380	gcgtt	4,23673
-70...-50	tgaeg	4,63388	380...400	tcat	4,19598
-60...-40	cgcgc	4,08437	430...450	tagtt	4,62317
-60...-40	cggaa	5,63737	440...460	gcggc	4,10319
-50...-30	cggaa	5,44443	460...480	tccgc	4,05704
-50...-30	ttccg	4,28122	480...500	tccag	-4,24253
-30...-10	aaagg	-4,72724	520...540	ctggg	-4,16399
-30...-10	aaggc	-4,58649	520...540	ttagt	4,3959
-30...-10	ccgga	4,25788	620...640	attat	4,67183
-30...-10	tccgg	4,9124	640...660	attct	4,3311
-30...-10	tgacg	5,30254	640...660	gatag	4,29612
-30...-10	ataaa[ag]	-5,02177	730...750	cggaa	4,05657
-40...-20	cctat	-4,55381	730...750	ttcgg	4,20068
-40...-20	cggaa	4,23417	770...790	tccaa	4,53685
-40...-20	gttgt	4,12955	790...810	gttcg	4,36969
-40...-20	tccgt	4,03029	870...890	gccaa	-4,02532
-40...-20	ttccg	4,64668	880...900	atgag	4,40802
-40...-20	c[ct]ataa	-4,42363	880...900	ctctg	-4,4515
-40...-20	[at][at]aaaa[ag][ag]	-4,28434	880...900	ggggc	-4,1903
-20...0	agtgg	4,77575	930...950	acaac	4,71736

Legend: **From-to** - position of the window where the motifs have been discovered. **Motif** - motif sequence itself. **Z-score** - The statistical significance of the motif. The positive values suggest that presence of the motif promotes the gene expression in non-lesional skin while negative values of Z-score suggest that motif acts in lesional skin. The absolute value of Z-score then indicates our confidence of influence of the motif.

Supplementary table 9. Association of motifs discovered by cisExpress with known TFs.

Motif	Source	E-value	Protein
GCATC	3D-footprint	3.6e-06	1gt0_C: OCTAMER-BINDING TRANSCRIPTION FACTOR 1
	3D-footprint	4.4e-05	1gt0_CD: OCTAMER-BINDING TRANSCRIPTION FACTOR 1
	HumanTF 1.0	1.5e-04	ATF4_DB: ATF4
	3D-footprint	3.6e-04	3ri4_D: Protein C-ets-1
	3D-footprint	3.8e-04	1bc7_C: PROTEIN (ETS-DOMAIN PROTEIN)
	3D-footprint	4.5e-04	4l0y_B: Protein C-ets-1

	3D-footprint	0.001	1e3o_C: OCTAMER-BINDING TRANSCRIPTION FACTOR 1
	HumanTF 1.0	0.001	GCM2_DBDB: GCM2
	HumanTF 1.0	0.001	GLIS1_DBDB: GLIS1
	HOCOMOCO v9	0.002	PO2F1_f1: PO2F1
TATGT	HumanTF 1.0	7.7e-06	NEUROG2_DBDB: NEUROG2
	HumanTF 1.0	9.0e-06	NEUROG2_full: NEUROG2
	JASPAR 2014	9.5e-06	MA0033: FOXL1
	HumanTF 1.0	2.8e-05	FOXJ3_DBDB_3: FOXJ3
	JASPAR 2014	3.1e-05	MA0025: NFIL3
	HOCOMOCO v9	3.1e-05	CDX1_f1: CDX1
	HumanTF 1.0	3.3e-05	BHLHE22_DBDB: BHLHE22
	HumanTF 1.0	3.5e-05	OLIG1_DBDB: OLIG1
	HumanTF 1.0	4.6e-05	OLIG2_DBDB: OLIG2
	HumanTF 1.0	5.9e-05	FOXB1_DBDB_3: FOXB1
CTCGG	3D-footprint	0.001	4eot_A: Transcription factor MafA
	HOCOMOCO v9	0.001	AP2B_f1: AP2B
	HOCOMOCO v9	0.002	AP2D_f1: AP2D
	HumanTF 1.0	0.004	TFAP2C_full_2: TFAP2C
	HumanTF 1.0	0.006	IRF5_full_2: IRF5
	HOCOMOCO v9	0.006	MAFK_si: MAFK
	HumanTF 1.0	0.006	HOXC13_DBDB_2: HOXC13
	HumanTF 1.0	0.007	HOXD13_DBDB_2: HOXD13
	HumanTF 1.0	0.007	HOXA13_full_2: HOXA13
	HumanTF 1.0	0.007	HOXB13_DBDB_2: HOXB13
CCAGG	HOCOMOCO v9	6.0e-06	TWST1_f1: TWST1
	HOCOMOCO v9	1.9e-05	COE1_f2: COE1
	HOCOMOCO v9	4.4e-05	STAT3_si: STAT3
	HOCOMOCO v9	6.4e-05	AP2C_f1: AP2C
	JASPAR 2014	9.3e-05	MA0154: EBF1
	HOCOMOCO v9	1.2e-04	AP2A_f2: AP2A
	JASPAR 2014	2.0e-04	MA0112: ESR1
	HOCOMOCO v9	2.9e-04	ESR1_do: ESR1
	HOCOMOCO v9	2.9e-04	ELK3_f1: ELK3
	JASPAR 2014	3.0e-04	MA0524: TFAP2C
CGACA	HumanTF 1.0	2.0e-05	ZBED1_DBDB: ZBED1
	3D-footprint	1.7e-04	1ozj_A: SMAD 3
	HOCOMOCO v9	3.6e-04	TGIF1_si: TGIF1
	3D-footprint	3.8e-04	1t2k_D: Cyclic-AMP-dependent transcription factor ATF-2
	3D-footprint	4.1e-04	1kb6_B: Vitamin D3 Receptor
	HumanTF 1.0	0.001	MEIS1_DBDB: MEIS1
	3D-footprint	0.001	1jnm_B: PROTO-ONCOGENE C-JUN
	HumanTF 1.0	0.002	MEIS2_DBDB_2: MEIS2

	HumanTF 1.0	0.002	MEIS3_DBDB_1: MEIS3
	3D-footprint	0.003	1ozj_AB: SMAD 3
GTCGT	HumanTF 1.0	1.3e-05	HOXC12_DBDB_2: HOXC12
	HumanTF 1.0	1.7e-05	HOXD12_DBDB_2: HOXD12
	HumanTF 1.0	2.2e-05	HOXC11_full_1: HOXC11
	HumanTF 1.0	2.6e-05	FOXO6_DBDB_3: FOXO6
	HumanTF 1.0	2.7e-05	HOXD11_DBDB_1: HOXD11
	HumanTF 1.0	5.3e-05	HOXC11_DBDB_1: HOXC11
	HumanTF 1.0	1.4e-04	HOXC10_DBDB_3: HOXC10
	HumanTF 1.0	1.8e-04	HOXA10_DBDB_1: HOXA10
	HumanTF 1.0	0.001	ZNF282_DBDB: ZNF282
	HumanTF 1.0	0.003	GLI2_DBDB_1: GLI2
CCGAT	HumanTF 1.0	2.5e-05	VENTX_DBDB_1: VENTX
	HumanTF 1.0	6.0e-05	OTX2_DBDB_1: OTX2
	HumanTF 1.0	7.4e-05	OTX1_DBDB_1: OTX1
	HumanTF 1.0	7.3e-04	VENTX_DBDB_2: VENTX
	HumanTF 1.0	0.003	BARX1_DBDB_1: BARX1
	3D-footprint	0.004	4uuv_M: ETS TRANSLOCATION VARIANT 4
	HumanTF 1.0	0.004	OTX1_DBDB_2: OTX1
	HumanTF 1.0	0.006	IRF5_full_2: IRF5
	HumanTF 1.0	0.006	BSX_DBDB: BSX
	HumanTF 1.0	0.007	CUX2_DBDB_2: CUX2
GCTTA	HOCOMOCO v9	1.8e-04	OTX1_f1: OTX1
	JASPAR 2014	0.001	MA0124: NKX3-1
	HOCOMOCO v9	0.001	GATA2_si: GATA2
	HumanTF 1.0	0.001	LHX2_DBDB_2: LHX2
	HOCOMOCO v9	0.002	CRX_si: CRX
	HumanTF 1.0	0.002	RFX3_DBDB_2: RFX3
	HumanTF 1.0	0.002	RHOXF1_DBDB_1: RHOXF1
	3D-footprint	0.002	3g73_A: Forkhead box protein M1
	3D-footprint	0.003	2uzk_A: FORKHEAD BOX PROTEIN O3A
	3D-footprint	0.003	3co6_C: Forkhead box protein O1
CGAAA	JASPAR 2016	0.003	FOXP3_DBDB / MA0850.1: FOXP3
	HumanTF 1.0	1.0e-05	IRF5_full_2: IRF5
	HumanTF 1.0	1.2e-05	HSFY2_DBDB_2: HSFY2
	HOCOMOCO v9	1.4e-05	E2F2_f1: E2F2
	HOCOMOCO v9	1.7e-05	EOMES_f1: EOMES
	HOCOMOCO v9	1.7e-05	E2F7_f1: E2F7
	HumanTF 1.0	2.1e-05	IRF7_DBDB_1: IRF7
	HOCOMOCO v9	2.1e-05	IRF9_f1: IRF9
	HumanTF 1.0	2.2e-05	IRF8_full: IRF8
	HOCOMOCO v9	2.4e-05	E2F3_si: E2F3
	HumanTF 1.0	2.5e-05	IRF8_DBDB: IRF8

CGATC	HOCOMOCO v9	7.2e-04	CUX1_f1: CUX1
	3D-footprint	0.003	4awl_A: NUCLEAR TRANSCRIPTION FACTOR Y SUBUNIT ALPHA
	HumanTF 1.0	0.003	CUX1_DBDB_1: CUX1
	HumanTF 1.0	0.003	CUX1_DBDB_2: CUX1
	HumanTF 1.0	0.004	CUX1_DBDB_3: CUX1
	HumanTF 1.0	0.005	CUX2_DBDB_2: CUX2
	HOCOMOCO v9	0.005	HXB1_f1: HXB1
	HumanTF 1.0	0.006	VENTX_DBDB_1: VENTX
	HumanTF 1.0	0.008	HOMEZ_DBDB: HOMEZ
	HumanTF 1.0	0.008	PAX7_full: PAX7
GAACA	HOCOMOCO v9	1.6e-07	GCR_si: GCR
	HOCOMOCO v9	2.2e-07	PRGR_f1: PRGR
	HOCOMOCO v9	1.7e-05	SOX9_f1: SOX9
	HOCOMOCO v9	2.1e-05	SOX4_f1: SOX4
	HumanTF 1.0	2.7e-05	SOX9_DBDB: SOX9
	JASPAR 2014	3.0e-05	MA0077: SOX9
	JASPAR 2014	3.4e-05	MA0007: AR
	HOCOMOCO v9	3.8e-05	PRGR_do: PRGR
	3D-footprint	3.9e-05	2c7a_AB: PROGESTERONE RECEPTOR
	HumanTF 1.0	5.2e-05	SOX2_full_1: SOX2
	HumanTF 1.0	0.001	FOXP3_DBDB / MA0850.1: FOXP3
ACGGA	3D-footprint	4.8e-05	1h89_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.8e-05	1h8a_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.8e-05	1h88_ABC: CCAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	1.4e-04	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	1.4e-04	2stt_A: ETS1
	3D-footprint	1.4e-04	4bqa_A: PROTEIN C-ETS-2
	HumanTF 1.0	1.4e-04	FOXG1_DBDB_2: FOXG1
	3D-footprint	1.8e-04	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	3.5e-04	4bnc_A: HUMAN ETV1
	3D-footprint	3.6e-04	4uno_A: ETS TRANSLOCATION VARIANT 5
CTACC	HumanTF 1.0	6.0e-06	ZNF784_full: ZNF784
	3D-footprint	0.002	4bnc_A: HUMAN ETV1
	3D-footprint	0.003	4iri_A: Transcriptional regulator ERG
	3D-footprint	0.003	2nnny_B: C-ets-1 protein
	HumanTF 1.0	0.004	SOX21_DBDB_1: SOX21
	HumanTF 1.0	0.005	GCM1_DBDB: GCM1
	HOCOMOCO v9	0.006	ZIC2_f1: ZIC2
	HOCOMOCO v9	0.006	SNAI1_f1: SNAI1
	3D-footprint	0.007	1h9d_C: CORE-BINDING FACTOR ALPHA SUBUNIT1

	HumanTF 1.0	0.008	GCM1_full_2: GCM1
GCACA	JASPAR 2014	8.4e-06	MA0058: MAX
	HumanTF 1.0	2.1e-05	MTF1_DB: MTF1
	HumanTF 1.0	3.3e-05	ZSCAN4_full: ZSCAN4
	HumanTF 1.0	6.9e-05	SOX9_full_1: SOX9
	HOCOMOCO v9	8.0e-05	MTF1_f1: MTF1
	JASPAR 2014	8.1e-05	MA0102: CEBPA
	HumanTF 1.0	9.9e-05	SOX8_DB: SOX8
	HOCOMOCO v9	1.2e-04	CEBPB_f1: CEBPB
	HumanTF 1.0	1.3e-04	SOX8_DB: SOX8
	3D-footprint	1.3e-04	1nlw_D: MAD PROTEIN
CGCCG	HumanTF 1.0	5.1e-04	ELK1_full_2: ELK1
	HOCOMOCO v9	9.2e-04	MBD2_si: MBD2
	HumanTF 1.0	0.002	FOXB1_DB: FOXB1
	HOCOMOCO v9	0.002	EGR4_f1: EGR4
	3D-footprint	0.003	1gtw_AB: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	0.004	2prt_A: Wilms tumor 1
	HOCOMOCO v9	0.004	EGR1_f2: EGR1
	HOCOMOCO v9	0.005	SP1_f1: SP1
	3D-footprint	0.005	4r2a_A: Early growth response protein 1
	HumanTF 1.0	0.006	YY2_DB: YY2
GTTCA	3D-footprint	2.5e-08	4cn3_D: RETINOIC ACID RECEPTOR RXR-ALPHA
	3D-footprint	2.9e-08	1kb2_B: Vitamin D3 Receptor
	HOCOMOCO v9	9.9e-07	NR1I2_si: NR1I2
	HOCOMOCO v9	4.2e-06	NR1I3_si: NR1I3
	HOCOMOCO v9	6.9e-06	VDR_f1: VDR
	3D-footprint	1.4e-05	4cn3_BC: RETINOIC ACID RECEPTOR RXR-ALPHA
	3D-footprint	1.4e-05	4cn3_AD: RETINOIC ACID RECEPTOR RXR-ALPHA
	3D-footprint	1.7e-05	3cbb_AB: Hepatocyte Nuclear Factor 4-alpha, DNA binding domain
	3D-footprint	1.7e-05	4cn5_AB: RETINOIC ACID RECEPTOR RXR-ALPHA
	3D-footprint	2.7e-05	1kb2_AB: Vitamin D3 Receptor
TGTAT	3D-footprint	9.6e-06	2c6y_AB: FORKHEAD BOX PROTEIN K2
	JASPAR 2014	2.5e-04	MA0033: FOXL1
	JASPAR 2014	0.001	MA0124: NKX3-1
	3D-footprint	0.001	1ozj_A: SMAD 3
	3D-footprint	0.003	2uzk_A: FORKHEAD BOX PROTEIN O3A
	3D-footprint	0.003	3qrf_G: Forkhead box protein P3
	3D-footprint	0.003	3l2c_A: Forkhead box protein O4
	3D-footprint	0.003	3co6_C: Forkhead box protein O1
	3D-footprint	0.003	3co7_F: Forkhead box protein O1

	3D-footprint	0.003	3coa_F: Forkhead box protein O1
ACGCC	3D-footprint	5.9e-06	2prt_A: Wilms tumor 1
	3D-footprint	1.4e-05	4r2a_A: Early growth response protein 1
	3D-footprint	1.7e-05	2jpa_A: Wilms tumor 1
	HumanTF 1.0	1.8e-05	SP8_DBDB: SP8
	3D-footprint	2.1e-05	2jp9_A: Wilms tumor 1
	HumanTF 1.0	2.1e-05	KLF16_DBDB: KLF16
	HumanTF 1.0	2.1e-05	KLF14_DBDB: KLF14
	HumanTF 1.0	2.7e-05	SP3_DBDB: SP3
	HumanTF 1.0	3.1e-05	EGR2_DBDB: EGR2
	HumanTF 1.0	3.2e-05	EGR1_full: EGR1
AGGGA	HOCOMOCO v9	1.6e-05	COE1_f2: COE1
	JASPAR 2014	6.8e-05	MA0154: EBF1
	HumanTF 1.0	6.9e-05	EBF1_full: EBF1
	3D-footprint	1.3e-04	2o61_B: Nuclear factor NF-kappa-B p105 subunit
	HOCOMOCO v9	1.9e-04	RFX1_f1: RFX1
	3D-footprint	2.6e-04	2pi0_ABCD: Interferon regulatory factor 3
	3D-footprint	3.0e-04	2o6g_EFGH: Interferon regulatory factor 3
	HOCOMOCO v9	3.2e-04	OTX2_si: OTX2
	3D-footprint	3.6e-04	1a3q_A: PROTEIN (NUCLEAR FACTOR KAPPA-B P52)
	HOCOMOCO v9	3.8e-04	HXD13_f1: HXD13
CTGGG	HOCOMOCO v9	1.1e-05	TWST1_f1: TWST1
	HOCOMOCO v9	2.6e-05	COE1_f2: COE1
	HOCOMOCO v9	4.9e-05	STAT4_si: STAT4
	HOCOMOCO v9	7.9e-05	AP2C_f1: AP2C
	HOCOMOCO v9	1.2e-04	AP2A_f2: AP2A
	JASPAR 2014	1.2e-04	MA0144: STAT3
	JASPAR 2014	1.3e-04	MA0154: EBF1
	3D-footprint	1.3e-04	2o61_B: Nuclear factor NF-kappa-B p105 subunit
	JASPAR 2014	3.7e-04	MA0524: TFAP2C
	HOCOMOCO v9	5.2e-04	STAT6_do: STAT6
TGGGT	HOCOMOCO v9	6.2e-06	GLI3_si: GLI3
	HOCOMOCO v9	6.6e-06	GLI2_f1: GLI2
	HOCOMOCO v9	6.7e-06	GLI1_f1: GLI1
	HumanTF 1.0	5.7e-05	GLI2_DBDB_1: GLI2
	HOCOMOCO v9	1.1e-04	BRCA1_f1: BRCA1
	3D-footprint	1.3e-04	2o61_B: Nuclear factor NF-kappa-B p105 subunit
	HOCOMOCO v9	1.6e-04	EGR3_f1: EGR3
	HOCOMOCO v9	1.7e-04	KLF3_f1: KLF3
	HumanTF 1.0	1.8e-04	ZNF143_DBDB: ZNF143
	HOCOMOCO v9	2.1e-04	ZN423_f1: ZN423
ACGAT	HumanTF 1.0	1.6e-05	HOMEZ_DBDB: HOMEZ

	HumanTF 1.0	1.0e-04	VENTX_DBDB_2: VENTX
	HumanTF 1.0	0.001	GLIS1_DBDB: GLIS1
	HumanTF 1.0	0.002	HOXD11_DBDB_1: HOXD11
	3D-footprint	0.003	3ri4_D: Protein C-ets-1
	HumanTF 1.0	0.003	VENTX_DBDB_1: VENTX
	3D-footprint	0.003	1bc7_C: PROTEIN (ETS-DOMAIN PROTEIN)
	3D-footprint	0.003	4l0y_B: Protein C-ets-1
	3D-footprint	0.003	1puB_B: Pre-B-cell leukemia transcription factor-1
	HumanTF 1.0	0.005	ESR1_DBDB: ESR1
TTCCT	3D-footprint	2.5e-08	3mfk_B: Protein C-ets-1
	3D-footprint	2.6e-08	1yo5_C: SAM pointed domain containing ets transcription factor
	3D-footprint	1.2e-07	2nny_B: C-ets-1 protein
	3D-footprint	1.2e-07	4lg0_B: Protein C-ets-1
	HOCOMOCO v9	1.3e-06	ETV4_f1: ETV4
	JASPAR 2014	1.6e-06	MA0598: EHF
	3D-footprint	1.7e-06	1a66_A: CORE NFATC1
	JASPAR 2014	2.5e-06	MA0156: FEV
	JASPAR 2014	3.7e-06	MA0081: SPIB
	HOCOMOCO v9	5.5e-06	FEV_f1: FEV
TACTC	JASPAR 2014	4.4e-04	MA0032: FOXC1
	HumanTF 1.0	5.7e-04	ZNF410_DBDB: ZNF410
	JASPAR 2014	0.001	MA0124: NKX3-1
	3D-footprint	0.001	1fos_EF: P55-C-FOS PROTO-ONCOGENE PROTEIN
	3D-footprint	0.002	1fos_GH: P55-C-FOS PROTO-ONCOGENE PROTEIN
	HOCOMOCO v9	0.002	SMRC1_f1: SMRC1
	HOCOMOCO v9	0.002	JUN_f1: JUN
	JASPAR 2014	0.002	MA0099: JUN::FOS
	3D-footprint	0.002	4eot_A: Transcription factor MafA
	3D-footprint	0.003	3cmy_A: Paired box protein Pax-3
	JASPAR 2016	0.004	MA0148.1:FOXA1
	JASPAR 2016	0.004	MA0148.2:FOXA1
CGGTA	HumanTF 1.0	5.6e-05	FOXI1_full_2: FOXI1
	HumanTF 1.0	3.1e-04	MEOX2_DBDB_2: MEOX2
	3D-footprint	5.0e-04	4bqa_A: PROTEIN C-ETS-2
	3D-footprint	0.001	1h9d_C: CORE-BINDING FACTOR ALPHA SUBUNIT1
	3D-footprint	0.001	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	0.002	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	0.002	4bnc_A: HUMAN ETV1
	3D-footprint	0.003	4iri_A: Transcriptional regulator ERG
	3D-footprint	0.004	4uv_M: ETS TRANSLOCATION VARIANT 4
	HumanTF 1.0	0.004	ZNF784_full: ZNF784
AGCGA	HOCOMOCO v9	3.6e-05	IRF9_f1: IRF9

	3D-footprint	1.3e-04	1cf7_B: PROTEIN (TRANSCRIPTION FACTOR DP-2)
	HumanTF 1.0	1.7e-04	FOXB1_DBDB_1: FOXB1
	HumanTF 1.0	2.5e-04	IRF7_DBDB_1: IRF7
	HOCOMOCO v9	3.4e-04	IRF3_f1: IRF3
	JASPAR 2014	8.9e-04	MA0051: IRF2
	3D-footprint	0.001	1cf7_AB: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HOCOMOCO v9	0.001	IRF7_f1: IRF7
	3D-footprint	0.001	1cf7_A: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HOCOMOCO v9	0.002	IRF2_f1: IRF2
ACCGG	HOCOMOCO v9	6.0e-06	ELK4_f1: ELK4
	HumanTF 1.0	6.0e-06	GRHL1_DBDB_2: GRHL1
	HumanTF 1.0	6.1e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.1e-06	FLI1_full_1: FLI1
	HumanTF 1.0	6.3e-06	ETV3_DBDB: ETV3
	HumanTF 1.0	6.5e-06	ETS1_full_1: ETS1
	HumanTF 1.0	6.6e-06	ERG_full_1: ERG
	HumanTF 1.0	6.6e-06	ELK4_DBDB: ELK4
	HumanTF 1.0	6.8e-06	ELK1_DBDB: ELK1
	HumanTF 1.0	6.9e-06	FEV_DBDB: FEV
CAGGA	3D-footprint	1.8e-06	4f6m_A: Transcriptional regulator Kaiso
	JASPAR 2014	2.6e-06	MA0156: FEV
	3D-footprint	1.1e-05	4lg0_AB: Forkhead box protein O1
	JASPAR 2014	1.8e-05	MA0475: FLI1
	HOCOMOCO v9	1.8e-05	ETS1_si: ETS1
	HOCOMOCO v9	1.9e-05	ELF3_f1: ELF3
	HOCOMOCO v9	3.1e-05	ELF2_f1: ELF2
	JASPAR 2014	3.6e-05	MA0098: Ets1
	HOCOMOCO v9	3.9e-05	ETV7_si: ETV7
	JASPAR 2014	4.1e-05	MA0598: EHF
CGCAA	3D-footprint	1.2e-07	2e42_A: CCAAT/enhancer-binding protein beta
	3D-footprint	1.8e-06	1gu4_AB: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	1.8e-06	2e43_AB: CCAAT/enhancer-binding protein beta
	3D-footprint	3.7e-06	1gtw_AB: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	4.7e-06	2e42_AB: CCAAT/enhancer-binding protein beta
	HumanTF 1.0	5.9e-06	CEBPG_full: CEBPG
	HumanTF 1.0	5.9e-06	CEBPG_DBDB: CEBPG
	HOCOMOCO v9	6.3e-06	AHR_si: AHR
	HumanTF 1.0	6.5e-06	CEBDP_DBDB: CEBPD
	HumanTF 1.0	6.7e-06	CEBPB_DBDB: CEBPB
CCTGG	HOCOMOCO v9	6.0e-06	TWST1_f1: TWST1

	HOCOMOCO v9	1.9e-05	COE1_f2: COE1
	HOCOMOCO v9	4.4e-05	STAT3_si: STAT3
	HOCOMOCO v9	6.4e-05	AP2C_f1: AP2C
	JASPAR 2014	9.3e-05	MA0154: EBF1
	HOCOMOCO v9	1.2e-04	AP2A_f2: AP2A
	JASPAR 2014	2.0e-04	MA0112: ESR1
	HOCOMOCO v9	2.9e-04	ESR1_do: ESR1
	HOCOMOCO v9	2.9e-04	ELK3_f1: ELK3
	JASPAR 2014	3.0e-04	MA0524: TFAP2C
TCCGT	3D-footprint	4.8e-05	1h89_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.8e-05	1h8a_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.8e-05	1h88_ABC: CCAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	1.4e-04	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	1.4e-04	2stt_A: ETS1
	3D-footprint	1.4e-04	4bqa_A: PROTEIN C-ETS-2
	HumanTF 1.0	1.4e-04	FOXG1_DB2_2: FOXG1
	3D-footprint	1.8e-04	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	3.5e-04	4bnc_A: HUMAN ETV1
	3D-footprint	3.6e-04	4uno_A: ETS TRANSLOCATION VARIANT 5
CTAAG	3D-footprint	3.6e-04	1srs_B: PROTEIN (SERUM RESPONSE FACTOR (SRF))
	HOCOMOCO v9	5.9e-04	OTX1_f1: OTX1
	HOCOMOCO v9	9.3e-04	FOXA2_f1: FOXA2
	JASPAR 2014	0.001	MA0124: NKX3-1
	3D-footprint	0.001	4rdv_A: Homeobox protein DLX-5
	3D-footprint	0.001	2lkx_A: Pituitary homeobox 3
	HOCOMOCO v9	0.001	GATA2_si: GATA2
	HumanTF 1.0	0.002	RFX3_DB2_2: RFX3
	HOCOMOCO v9	0.002	PDX1_do: PDX1
	3D-footprint	0.002	4j19_B: Homeobox-containing protein 1
	HOCOMOCO v9	0.005	FOXA1_f1: FOXA1
CGGAA	3D-footprint	2.7e-08	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	2.8e-08	4bqa_A: PROTEIN C-ETS-2
	3D-footprint	3.8e-08	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	1.2e-07	4bnc_A: HUMAN ETV1
	3D-footprint	1.3e-07	4iri_A: Transcriptional regulator ERG
	HOCOMOCO v9	2.4e-06	ELK1_f1: ELK1
	HOCOMOCO v9	5.8e-06	GABP1+GABP2_f1: GABP1+GABP2
	HumanTF 1.0	5.9e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.2e-06	ELK1_DB2: ELK1
	HumanTF 1.0	6.3e-06	FLI1_full_1: FLI1
TCGCG	3D-footprint	3.5e-08	1cf7_B: PROTEIN (TRANSCRIPTION FACTOR DP-

		2)
	3D-footprint	8.0e-07 1cf7_AB: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	3D-footprint	9.5e-07 1cf7_A: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HOCOMOCO v9	1.1e-05 E2F2_f1: E2F2
	HOCOMOCO v9	1.4e-05 E2F3_si: E2F3
	HumanTF 1.0	1.7e-05 ZBED1_DBDB: ZBED1
	HOCOMOCO v9	1.7e-05 E2F7_f1: E2F7
	JASPAR 2014	3.2e-05 MA0527: ZBTB33
	HOCOMOCO v9	9.9e-05 E2F5_do: E2F5
	HumanTF 1.0	2.9e-04 GLIS2_DBDB: GLIS2
TGTCA	HOCOMOCO v9	1.2e-07 TGIF1_si: TGIF1
	3D-footprint	1.3e-07 1t2k_D: Cyclic-AMP-dependent transcription factor ATF-2
	HumanTF 1.0	7.5e-07 MEIS1_DBDB: MEIS1
	HumanTF 1.0	1.6e-06 MEIS2_DBDB_2: MEIS2
	HumanTF 1.0	1.7e-06 MEIS3_DBDB_1: MEIS3
	HumanTF 1.0	1.4e-05 TGIF1_DBDB: TGIF1
	HumanTF 1.0	1.4e-05 PKNOX1_DBDB: PKNOX1
	HumanTF 1.0	1.4e-05 PKNOX2_DBDB: PKNOX2
	HumanTF 1.0	1.4e-05 TGIF2LX_full: TGIF2LX
	HumanTF 1.0	1.4e-05 TGIF2_DBDB: TGIF2
AGACT	3D-footprint	1.3e-07 1mhd_B: SMAD3
	3D-footprint	1.3e-04 1ozj_A: SMAD 3
	3D-footprint	1.3e-04 1fos_E: P55-C-FOS PROTO-ONCOGENE PROTEIN
	3D-footprint	3.6e-04 4aa6_E: ESTROGEN RECEPTOR
	HOCOMOCO v9	4.9e-04 MAFG_si: MAFG
	3D-footprint	0.001 1fos_EF: P55-C-FOS PROTO-ONCOGENE PROTEIN
	HOCOMOCO v9	0.001 NF2L1_f1: NF2L1
	HOCOMOCO v9	0.001 PRGR_do: PRGR
	3D-footprint	0.002 1fos_GH: P55-C-FOS PROTO-ONCOGENE PROTEIN
	HOCOMOCO v9	0.002 SMAD4_si: SMAD4
CGAGA	HumanTF 1.0	3.3e-05 HOXA13_full_2: HOXA13
	JASPAR 2014	3.3e-05 MA0527: ZBTB33
	3D-footprint	0.001 4h10_A: Aryl hydrocarbon receptor nuclear translocator-like protein 1
	3D-footprint	0.001 1cf7_B: PROTEIN (TRANSCRIPTION FACTOR DP-2)
	3D-footprint	0.003 1cf7_A: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HOCOMOCO v9	0.004 HES1_f1: HES1
	HumanTF 1.0	0.006 HOXC13_DBDB_2: HOXC13
	3D-footprint	0.006 1cf7_AB: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HumanTF 1.0	0.007 HOXD13_DBDB_2: HOXD13

	HOCOMOCO v9	0.007	RARA_f2: RARA
GACGC	HOCOMOCO v9	1.7e-04	ATF3_f1: ATF3
	3D-footprint	1.8e-04	1jnm_B: PROTO-ONCOGENE C-JUN
	HOCOMOCO v9	2.2e-04	HEN1_si: HEN1
	HumanTF 1.0	2.7e-04	PROX1_DB: PROX1
	HumanTF 1.0	8.4e-04	ATF4_DB: ATF4
	HumanTF 1.0	9.3e-04	HINFP1_full_1: HINFP1
	HOCOMOCO v9	0.002	CREB1_f1: CREB1
	JASPAR 2014	0.002	MA0018: CREB1
	3D-footprint	0.002	1jnm_AB: PROTO-ONCOGENE C-JUN
	HOCOMOCO v9	0.002	AHR_si: AHR
TGACG	3D-footprint	3.8e-08	1jnm_B: PROTO-ONCOGENE C-JUN
	3D-footprint	1.6e-06	1jnm_AB: PROTO-ONCOGENE C-JUN
	HOCOMOCO v9	1.6e-06	CREB1_f1: CREB1
	HOCOMOCO v9	1.8e-06	ATF2+ATF4_f1: ATF2+ATF4
	JASPAR 2014	2.3e-06	MA0018: CREB1
	HOCOMOCO v9	3.6e-06	ATF1_si: ATF1
	HOCOMOCO v9	8.7e-06	CREM_f1: CREM
	HOCOMOCO v9	9.8e-06	ATF6A_si: ATF6A
	HumanTF 1.0	1.4e-05	JDP2_DB: JDP2
	HumanTF 1.0	1.4e-05	JDP2_full_2: JDP2
CGCGC	3D-footprint	7.8e-07	1cf7_AB: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	3D-footprint	8.0e-07	1cf7_A: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HOCOMOCO v9	6.4e-06	E2F2_f1: E2F2
	HOCOMOCO v9	1.7e-05	E2F7_f1: E2F7
	HOCOMOCO v9	3.5e-05	AP2D_f1: AP2D
	HOCOMOCO v9	1.0e-04	E2F5_do: E2F5
	3D-footprint	1.6e-04	1cf7_B: PROTEIN (TRANSCRIPTION FACTOR DP-2)
	HOCOMOCO v9	2.1e-04	E2F3_si: E2F3
	3D-footprint	0.001	1nlw_D: MAD PROTEIN
	3D-footprint	0.001	1nkp_E: Max protein
CGGAA	3D-footprint	2.7e-08	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	2.8e-08	4bqa_A: PROTEIN C-ETS-2
	3D-footprint	3.8e-08	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	1.2e-07	4bnc_A: HUMAN ETV1
	3D-footprint	1.3e-07	4iri_A: Transcriptional regulator ERG
	HOCOMOCO v9	2.4e-06	ELK1_f1: ELK1
	HOCOMOCO v9	5.8e-06	GABP1+GABP2_f1: GABP1+GABP2
	HumanTF 1.0	5.9e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.2e-06	ELK1_DB: ELK1
	HumanTF 1.0	6.3e-06	FLI1_full_1: FLI1

CGGAA	3D-footprint	2.7e-08	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	2.8e-08	4bqa_A: PROTEIN C-ETS-2
	3D-footprint	3.8e-08	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	1.2e-07	4bnc_A: HUMAN ETV1
	3D-footprint	1.3e-07	4iri_A: Transcriptional regulator ERG
	HOCOMOCO v9	2.4e-06	ELK1_f1: ELK1
	HOCOMOCO v9	5.8e-06	GABP1+GABP2_f1: GABP1+GABP2
	HumanTF 1.0	5.9e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.2e-06	ELK1_DBDB: ELK1
	HumanTF 1.0	6.3e-06	FLI1_full_1: FLI1
TTCCG	3D-footprint	2.7e-08	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	2.8e-08	4bqa_A: PROTEIN C-ETS-2
	3D-footprint	3.8e-08	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	1.2e-07	4bnc_A: HUMAN ETV1
	3D-footprint	1.3e-07	4iri_A: Transcriptional regulator ERG
	HOCOMOCO v9	2.4e-06	ELK1_f1: ELK1
	HOCOMOCO v9	5.8e-06	GABP1+GABP2_f1: GABP1+GABP2
	HumanTF 1.0	5.9e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.2e-06	ELK1_DBDB: ELK1
	HumanTF 1.0	6.3e-06	FLI1_full_1: FLI1
AAAGG	HOCOMOCO v9	4.2e-06	COT1_si: COT1
	HOCOMOCO v9	4.6e-06	NR4A3_f1: NR4A3
	HumanTF 1.0	9.9e-06	NR4A2_full_3: NR4A2
	HOCOMOCO v9	1.2e-05	COT2_f1: COT2
	HOCOMOCO v9	1.4e-05	RXRG_f1: RXRG
	HumanTF 1.0	1.6e-05	TCF7L1_full: TCF7L1
	HumanTF 1.0	2.1e-05	RXRG_full: RXRG
	HumanTF 1.0	2.1e-05	NR2F6_DBDB_2: NR2F6
	HumanTF 1.0	2.1e-05	RXRA_full_1: RXRA
	HumanTF 1.0	2.1e-05	RXRB_DBDB: RXRB
AAGGC	HumanTF 1.0	1.7e-05	PRDM4_full: PRDM4
	3D-footprint	3.7e-05	1hf0_AB: OCTAMER-BINDING TRANSCRIPTION FACTOR 1
	HOCOMOCO v9	6.4e-05	NR5A2_f1: NR5A2
	JASPAR 2014	2.4e-04	MA0083: SRF
	HumanTF 1.0	2.7e-04	PROX1_DBDB: PROX1
	HOCOMOCO v9	3.6e-04	STF1_f1: STF1
	3D-footprint	3.7e-04	1srs_B: PROTEIN (SERUM RESPONSE FACTOR (SRF))
	HOCOMOCO v9	0.001	TF7L2_f1: TF7L2
	HOCOMOCO v9	0.002	E2F7_f1: E2F7
	HOCOMOCO v9	0.002	ERR2_f1: ERR2
CCGGA	3D-footprint	2.7e-08	2stt_A: ETS1
	3D-footprint	1.1e-06	1dux_F: ETS-DOMAIN PROTEIN ELK-1

	HOCOMOCO v9	1.3e-06	MECP2_f1: MECP2
	HOCOMOCO v9	2.5e-06	ELK1_f1: ELK1
	HumanTF 1.0	5.8e-06	ELK1_full_1: ELK1
	HumanTF 1.0	5.9e-06	GABPA_full: GABPA
	HumanTF 1.0	6.0e-06	FLI1_full_1: FLI1
	HOCOMOCO v9	6.0e-06	ELK4_f1: ELK4
	HumanTF 1.0	6.0e-06	ELK4_DBDB: ELK4
	HumanTF 1.0	6.0e-06	ELK3_DBDB: ELK3
TCCGG	3D-footprint	2.7e-08	2stt_A: ETS1
	3D-footprint	1.1e-06	1dux_F: ETS-DOMAIN PROTEIN ELK-1
	HOCOMOCO v9	1.3e-06	MECP2_f1: MECP2
	HOCOMOCO v9	2.5e-06	ELK1_f1: ELK1
	HumanTF 1.0	5.8e-06	ELK1_full_1: ELK1
	HumanTF 1.0	5.9e-06	GABPA_full: GABPA
	HumanTF 1.0	6.0e-06	FLI1_full_1: FLI1
	HOCOMOCO v9	6.0e-06	ELK4_f1: ELK4
	HumanTF 1.0	6.0e-06	ELK4_DBDB: ELK4
	HumanTF 1.0	6.0e-06	ELK3_DBDB: ELK3
TGACG	3D-footprint	3.8e-08	1jnm_B: PROTO-ONCOGENE C-JUN
	3D-footprint	1.6e-06	1jnm_AB: PROTO-ONCOGENE C-JUN
	HOCOMOCO v9	1.6e-06	CREB1_f1: CREB1
	HOCOMOCO v9	1.8e-06	ATF2+ATF4_f1: ATF2+ATF4
	JASPAR 2014	2.3e-06	MA0018: CREB1
	HOCOMOCO v9	3.6e-06	ATF1_si: ATF1
	HOCOMOCO v9	8.7e-06	CREM_f1: CREM
	HOCOMOCO v9	9.8e-06	ATF6A_si: ATF6A
	HumanTF 1.0	1.4e-05	JDP2_DBDB_2: JDP2
	HumanTF 1.0	1.4e-05	JDP2_full_2: JDP2
CCTAT	HOCOMOCO v9	2.0e-04	PPARG_si: PPARG
	3D-footprint	3.6e-04	1srs_B: PROTEIN (SERUM RESPONSE FACTOR (SRF))
	HOCOMOCO v9	9.4e-04	GATA3_si: GATA3
	HOCOMOCO v9	0.002	GATA2_si: GATA2
	3D-footprint	0.003	1hbz_D: SERUM RESPONSE FACTOR
	HOCOMOCO v9	0.003	NR1D1_f1: NR1D1
	HumanTF 1.0	0.004	ZNF784_full: ZNF784
	3D-footprint	0.004	1srs_AB: PROTEIN (SERUM RESPONSE FACTOR (SRF))
	3D-footprint	0.005	1mhd_AB: SMAD3
	3D-footprint	0.005	1n6j_AB: Myocyte-specific enhancer factor 2B
CGGAA	3D-footprint	2.7e-08	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	2.8e-08	4bqa_A: PROTEIN C-ETS-2
	3D-footprint	3.8e-08	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	1.2e-07	4bnc_A: HUMAN ETV1

	3D-footprint	1.3e-07	4iri_A: Transcriptional regulator ERG
	HOCOMOCO v9	2.4e-06	ELK1_f1: ELK1
	HOCOMOCO v9	5.8e-06	GABP1+GABP2_f1: GABP1+GABP2
	HumanTF 1.0	5.9e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.2e-06	ELK1_DBDB: ELK1
	HumanTF 1.0	6.3e-06	FLI1_full_1: FLI1
GTCGT	HumanTF 1.0	1.3e-05	HOXC12_DBDB_2: HOXC12
	HumanTF 1.0	1.7e-05	HOXD12_DBDB_2: HOXD12
	HumanTF 1.0	2.2e-05	HOXC11_full_1: HOXC11
	HumanTF 1.0	2.6e-05	FOXO6_DBDB_3: FOXO6
	HumanTF 1.0	2.7e-05	HOXD11_DBDB_1: HOXD11
	HumanTF 1.0	5.3e-05	HOXC11_DBDB_1: HOXC11
	HumanTF 1.0	1.4e-04	HOXC10_DBDB_3: HOXC10
	HumanTF 1.0	1.8e-04	HOXA10_DBDB_1: HOXA10
	HumanTF 1.0	0.001	ZNF282_DBDB: ZNF282
	HumanTF 1.0	0.003	GLI2_DBDB_1: GLI2
TCCGT	3D-footprint	4.8e-05	1h89_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.8e-05	1h8a_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.8e-05	1h88_ABC: CCAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	1.4e-04	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	1.4e-04	2stt_A: ETS1
	3D-footprint	1.4e-04	4bqa_A: PROTEIN C-ETS-2
	HumanTF 1.0	1.4e-04	FOXG1_DBDB_2: FOXG1
	3D-footprint	1.8e-04	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	3.5e-04	4bnc_A: HUMAN ETV1
	3D-footprint	3.6e-04	4uno_A: ETS TRANSLOCATION VARIANT 5
TTCCG	3D-footprint	2.7e-08	2o93_M: actor of activated T-cells, cytoplasmic 2
	3D-footprint	2.8e-08	4bqa_A: PROTEIN C-ETS-2
	3D-footprint	3.8e-08	1bc8_C: PROTEIN (SAP-1 ETS DOMAIN)
	3D-footprint	1.2e-07	4bnc_A: HUMAN ETV1
	3D-footprint	1.3e-07	4iri_A: Transcriptional regulator ERG
	HOCOMOCO v9	2.4e-06	ELK1_f1: ELK1
	HOCOMOCO v9	5.8e-06	GABP1+GABP2_f1: GABP1+GABP2
	HumanTF 1.0	5.9e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.2e-06	ELK1_DBDB: ELK1
	HumanTF 1.0	6.3e-06	FLI1_full_1: FLI1
AGTGG	HumanTF 1.0	4.1e-06	NKX3-1_full: NKX3-1
	HOCOMOCO v9	6.3e-06	NKX32_f1: NKX32
	HumanTF 1.0	7.5e-06	NKX2-3_DBDB: NKX2-3
	HumanTF 1.0	7.6e-06	NKX3-2_DBDB: NKX3-2
	HumanTF 1.0	1.4e-05	NKX2-3_full: NKX2-3

	HOCOMOCO v9	1.4e-05	EGR3_f1: EGR3
	JASPAR 2014	5.7e-05	MA0475: FLI1
	HumanTF 1.0	6.4e-05	NKX2-8_full: NKX2-8
	HOCOMOCO v9	6.5e-05	ETS2_f1: ETS2
	JASPAR 2014	8.9e-05	MA0098: Ets1
TGACG	3D-footprint	3.8e-08	1jnm_B: PROTO-ONCOGENE C-JUN
	3D-footprint	1.6e-06	1jnm_AB: PROTO-ONCOGENE C-JUN
	HOCOMOCO v9	1.6e-06	CREB1_f1: CREB1
	HOCOMOCO v9	1.8e-06	ATF2+ATF4_f1: ATF2+ATF4
	JASPAR 2014	2.3e-06	MA0018: CREB1
	HOCOMOCO v9	3.6e-06	ATF1_si: ATF1
	HOCOMOCO v9	8.7e-06	CREM_f1: CREM
	HOCOMOCO v9	9.8e-06	ATF6A_si: ATF6A
	HumanTF 1.0	1.4e-05	JDP2_DBDB_2: JDP2
	HumanTF 1.0	1.4e-05	JDP2_full_2: JDP2
CCGGAA	HOCOMOCO v9	6.9e-09	ELK1_f1: ELK1
	HumanTF 1.0	2.6e-08	ELK1_full_1: ELK1
	HumanTF 1.0	2.8e-08	FLI1_full_1: FLI1
	HumanTF 1.0	2.8e-08	ELK1_DBDB: ELK1
	HumanTF 1.0	2.9e-08	ELK3_DBDB: ELK3
	HumanTF 1.0	3.1e-08	ELK4_DBDB: ELK4
	HumanTF 1.0	3.2e-08	ERG_full_1: ERG
	HumanTF 1.0	3.2e-08	ERF_DBDB: ERF
	HumanTF 1.0	3.2e-08	GABPA_full: GABPA
	HumanTF 1.0	4.0e-08	ERG_DBDB_1: ERG
AATGG	HOCOMOCO v9	1.3e-06	NANOG_f1: NANOG
	HumanTF 1.0	9.6e-06	YY2_DBDB: YY2
	HumanTF 1.0	9.8e-06	YY1_full: YY1
	JASPAR 2014	1.4e-05	MA0077: SOX9
	3D-footprint	1.4e-05	1ubd_C: PROTEIN (YY1 ZINC FINGER DOMAIN)
	HOCOMOCO v9	1.7e-05	SOX9_f1: SOX9
	HumanTF 1.0	1.8e-05	E2F4_DBDB_1: E2F4
	HOCOMOCO v9	2.0e-05	NFAC1_si: NFAC1
	HumanTF 1.0	3.7e-05	YY2_full: YY2
	HumanTF 1.0	4.4e-05	SOX9_DBDB: SOX9
CAGAC	HOCOMOCO v9	2.0e-06	SMAD4_si: SMAD4
	HOCOMOCO v9	4.1e-06	SMAD3_f1: SMAD3
	HOCOMOCO v9	1.9e-05	SMAD1_si: SMAD1
	JASPAR 2014	3.1e-05	MA0513: SMAD2::SMAD3::SMAD4
	HOCOMOCO v9	4.9e-05	HAND1_si: HAND1
	JASPAR 2014	1.2e-04	MA0106: TP53
	3D-footprint	1.3e-04	1ozj_A: SMAD 3
	HOCOMOCO v9	1.6e-04	SMAD2_si: SMAD2

	JASPAR 2014	3.3e-04	MA0002: RUNX1
	3D-footprint	3.6e-04	1mhd_B: SMAD3
CAGCA	HOCOMOCO v9	7.3e-07	MAF_f1: MAF
	3D-footprint	4.7e-06	4eot_A: Transcription factor MafA
	HumanTF 1.0	1.5e-05	NRL_DBD: NRL
	HumanTF 1.0	1.6e-05	MAFK_DBD_1: MAFK
	HumanTF 1.0	1.8e-05	MAFK_full_1: MAFK
	HOCOMOCO v9	1.9e-05	NFE2_f2: NFE2
	HumanTF 1.0	3.1e-05	MAFF_DBD: MAFF
	JASPAR 2014	3.1e-05	MA0501: NFE2::MAF
	JASPAR 2014	3.1e-05	MA0496: MAFK
	JASPAR 2014	3.2e-05	MA0150: Nfe2l2
GCCAT	HumanTF 1.0	9.6e-06	YY2_DBD: YY2
	HOCOMOCO v9	1.0e-05	TYY1_f2: TYY1
	HumanTF 1.0	1.1e-05	YY2_full: YY2
	HumanTF 1.0	1.3e-05	YY1_full: YY1
	JASPAR 2014	1.5e-05	MA0095: YY1
	HumanTF 1.0	1.8e-05	E2F4_DBD_1: E2F4
	HumanTF 1.0	5.7e-05	E2F2_DBD_1: E2F2
	HOCOMOCO v9	6.9e-05	RFX3_f1: RFX3
	3D-footprint	7.0e-05	1gtw_B: CAAT/ENHANCER BINDING PROTEIN BETA
	HumanTF 1.0	8.1e-05	E2F2_DBD_3: E2F2
GGCGG	HOCOMOCO v9	8.8e-06	SP1_f1: SP1
	HOCOMOCO v9	9.6e-06	EGR1_f2: EGR1
	HumanTF 1.0	1.1e-05	YY2_full: YY2
	HOCOMOCO v9	1.2e-05	E2F6_f1: E2F6
	HOCOMOCO v9	1.2e-05	TYY1_f2: TYY1
	HOCOMOCO v9	1.2e-05	EGR2_si: EGR2
	HumanTF 1.0	1.2e-05	YY2_DBD: YY2
	HumanTF 1.0	1.4e-05	E2F8_DBD: E2F8
	JASPAR 2014	1.8e-05	MA0471: E2F6
	HOCOMOCO v9	1.9e-05	KLF6_si: KLF6
TCACG	3D-footprint	2.6e-08	4h10_A: Aryl hydrocarbon receptor nuclear translocator-like protein 1
	3D-footprint	9.5e-07	4h10_AB: Aryl hydrocarbon receptor nuclear translocator-like protein 1
	HOCOMOCO v9	1.6e-06	TFEB_f1: TFEB
	HOCOMOCO v9	1.7e-06	BHE40_f2: BHE40
	HOCOMOCO v9	3.9e-06	USF1_f1: USF1
	HumanTF 1.0	5.8e-06	ARNTL_DBD: ARNTL
	HumanTF 1.0	6.0e-06	MLXIPL_full: MLXIPL
	HumanTF 1.0	6.0e-06	MLX_full: MLX
	HumanTF 1.0	6.1e-06	SREBF2_DBD: SREBF2

	HumanTF 1.0	7.0e-06	BHLHE41_full: BHLHE41
AAGAT	HumanTF 1.0	1.9e-05	TCF7L1_full: TCF7L1
	HOCOMOCO v9	2.5e-05	TYY1_f2: TYY1
	HOCOMOCO v9	3.3e-05	EVI1_f1: EVI1
	HumanTF 1.0	4.8e-05	LEF1_DBDB: LEF1
	JASPAR 2014	9.7e-05	MA0095: YY1
	HOCOMOCO v9	3.4e-04	CEBPE_f1: CEBPE
	HOCOMOCO v9	0.001	GATA6_f2: GATA6
	JASPAR 2014	0.001	MA0488: JUN
	3D-footprint	0.001	3rkq_B: Homeobox protein Nkx-2.5
	HOCOMOCO v9	0.001	GATA2_si: GATA2
CACAG	JASPAR 2014	3.2e-05	MA0002: RUNX1
	HumanTF 1.0	5.2e-05	ZIC1_full: ZIC1
	3D-footprint	8.5e-05	3nbn_AD: Recombining binding protein suppressor of hairless
	HOCOMOCO v9	1.2e-04	RUNX1_f1: RUNX1
	HumanTF 1.0	1.3e-04	FOXB1_DBDB_1: FOXB1
	HOCOMOCO v9	1.5e-04	PEBB_f1: PEBB
	HOCOMOCO v9	2.1e-04	GFI1_f1: GFI1
	HumanTF 1.0	2.8e-04	ZIC4_DBDB: ZIC4
	HOCOMOCO v9	3.0e-04	TFAP4_si: TFAP4
	HOCOMOCO v9	3.8e-04	TGIF1_si: TGIF1
GATGGC	HOCOMOCO v9	1.7e-07	TYY1_f2: TYY1
	HOCOMOCO v9	8.3e-07	ZBTB4_si: ZBTB4
	JASPAR 2014	8.8e-07	MA0095: YY1
	HOCOMOCO v9	8.0e-06	NDF1_f1: NDF1
	HumanTF 1.0	2.5e-05	YY2_full: YY2
	HOCOMOCO v9	4.9e-05	HXB1_f1: HXB1
	HOCOMOCO v9	6.1e-05	HXA1_f1: HXA1
	HumanTF 1.0	1.1e-04	YY2_DBDB: YY2
	HumanTF 1.0	1.4e-04	YY1_full: YY1
	HOCOMOCO v9	1.5e-04	TAL1_f1: TAL1
TGGCGG	HumanTF 1.0	5.8e-08	YY2_full: YY2
	HOCOMOCO v9	6.3e-08	TYY1_f2: TYY1
	HumanTF 1.0	6.8e-08	YY2_DBDB: YY2
	HumanTF 1.0	8.6e-08	E2F8_DBDB: E2F8
	HumanTF 1.0	1.1e-07	YY1_full: YY1
	HumanTF 1.0	1.5e-07	E2F7_DBDB: E2F7
	JASPAR 2014	3.9e-07	MA0095: YY1
	HOCOMOCO v9	1.5e-06	E2F4_do: E2F4
	HOCOMOCO v9	1.7e-06	TFDP1_f1: TFDP1
	HOCOMOCO v9	3.3e-06	E2F1_f2: E2F1
AGCTC	HumanTF 1.0	5.2e-05	POU6F2_DBDB_1: POU6F2

	HOCOMOCO v9	2.7e-04	PO4F2_si: PO4F2
	HumanTF 1.0	4.1e-04	POU6F2_DBDB_2: POU6F2
	HOCOMOCO v9	8.5e-04	TEAD4_f1: TEAD4
	HOCOMOCO v9	0.002	MYF6_f1: MYF6
	HOCOMOCO v9	0.003	RARA_f1: RARA
	3D-footprint	0.003	4nqa_I: Liver X nuclear receptor beta
	HOCOMOCO v9	0.003	PPARA_f1: PPARA
	3D-footprint	0.003	4cn7_F: RETINOIC ACID RECEPTOR RXR-ALPHA
	HumanTF 1.0	0.004	TFAP4_full: TFAP4
AAGATG	HOCOMOCO v9	1.5e-07	TYY1_f2: TYY1
	JASPAR 2014	8.2e-07	MA0095: YY1
	3D-footprint	1.3e-05	3ri4_D: Protein C-ets-1
	JASPAR 2014	1.4e-05	MA0488: JUN
	3D-footprint	1.4e-05	1bc7_C: PROTEIN (ETS-DOMAIN PROTEIN)
	3D-footprint	1.8e-05	4l0y_B: Protein C-ets-1
	3D-footprint	6.8e-05	4hca_A: Trans-acting T-cell-specific transcription factor GATA-3
	HOCOMOCO v9	8.4e-05	TFE2_f2: TFE2
	HumanTF 1.0	1.0e-04	YY2_full: YY2
	HOCOMOCO v9	1.1e-04	TAL1_f1: TAL1
GATGGC	HOCOMOCO v9	1.7e-07	TYY1_f2: TYY1
	HOCOMOCO v9	8.3e-07	ZBTB4_si: ZBTB4
	JASPAR 2014	8.8e-07	MA0095: YY1
	HOCOMOCO v9	8.0e-06	NDF1_f1: NDF1
	HumanTF 1.0	2.5e-05	YY2_full: YY2
	HOCOMOCO v9	4.9e-05	HXB1_f1: HXB1
	HOCOMOCO v9	6.1e-05	HXA1_f1: HXA1
	HumanTF 1.0	1.1e-04	YY2_DBDB: YY2
	HumanTF 1.0	1.4e-04	YY1_full: YY1
	HOCOMOCO v9	1.5e-04	TAL1_f1: TAL1
TGGCGG	HumanTF 1.0	5.8e-08	YY2_full: YY2
	HOCOMOCO v9	6.3e-08	TYY1_f2: TYY1
	HumanTF 1.0	6.8e-08	YY2_DBDB: YY2
	HumanTF 1.0	8.6e-08	E2F8_DBDB: E2F8
	HumanTF 1.0	1.1e-07	YY1_full: YY1
	HumanTF 1.0	1.5e-07	E2F7_DBDB: E2F7
	JASPAR 2014	3.9e-07	MA0095: YY1
	HOCOMOCO v9	1.5e-06	E2F4_do: E2F4
	HOCOMOCO v9	1.7e-06	TFDP1_f1: TFDP1
	HOCOMOCO v9	3.3e-06	E2F1_f2: E2F1
CACAG	JASPAR 2014	3.2e-05	MA0002: RUNX1
	HumanTF 1.0	5.2e-05	ZIC1_full: ZIC1
	3D-footprint	8.5e-05	3nbn_AD: Recombining binding protein suppressor of hairless

	HOCOMOCO v9	1.2e-04	RUNX1_f1: RUNX1
	HumanTF 1.0	1.3e-04	FOXB1_DBDB_1: FOXB1
	HOCOMOCO v9	1.5e-04	PEBB_f1: PEBB
	HOCOMOCO v9	2.1e-04	GFI1_f1: GFI1
	HumanTF 1.0	2.8e-04	ZIC4_DBDB: ZIC4
	HOCOMOCO v9	3.0e-04	TFAP4_si: TFAP4
	HOCOMOCO v9	3.8e-04	TGIF1_si: TGIF1
CTGCT	HOCOMOCO v9	6.1e-05	MYOG_f1: MYOG
	3D-footprint	1.3e-04	4f2j_C: Zinc finger protein 217
	HOCOMOCO v9	2.9e-04	ELF2_f1: ELF2
	JASPAR 2014	5.3e-04	MA0140: TAL1::GATA1
	HOCOMOCO v9	7.1e-04	TEAD3_si: TEAD3
	HOCOMOCO v9	0.001	MAF_f1: MAF
	HumanTF 1.0	0.001	NHLH1_full: NHLH1
	HumanTF 1.0	0.001	SNAI2_DBDB: SNAI2
	3D-footprint	0.001	4is1_C: Zinc finger protein 217
	HOCOMOCO v9	0.002	HEN1_si: HEN1
ACAAT	HOCOMOCO v9	7.5e-07	SOX5_f1: SOX5
	HOCOMOCO v9	1.2e-06	SOX13_f1: SOX13
	HOCOMOCO v9	1.5e-06	SOX15_f1: SOX15
	HOCOMOCO v9	1.5e-06	MSX2_f1: MSX2
	HumanTF 1.0	3.8e-06	SOX9_DBDB: SOX9
	JASPAR 2014	4.5e-06	MA0077: SOX9
	HumanTF 1.0	5.9e-06	FOXK1_DBDB: FOXK1
	HOCOMOCO v9	6.1e-06	SOX9_f1: SOX9
	JASPAR 2014	6.4e-06	MA0084: SRY
	3D-footprint	1.0e-05	2c6y_AB: FORKHEAD BOX PROTEIN K2
CTGCT	HOCOMOCO v9	6.1e-05	MYOG_f1: MYOG
	3D-footprint	1.3e-04	4f2j_C: Zinc finger protein 217
	HOCOMOCO v9	2.9e-04	ELF2_f1: ELF2
	JASPAR 2014	5.3e-04	MA0140: TAL1::GATA1
	HOCOMOCO v9	7.1e-04	TEAD3_si: TEAD3
	HOCOMOCO v9	0.001	MAF_f1: MAF
	HumanTF 1.0	0.001	NHLH1_full: NHLH1
	HumanTF 1.0	0.001	SNAI2_DBDB: SNAI2
	3D-footprint	0.001	4is1_C: Zinc finger protein 217
	HOCOMOCO v9	0.002	HEN1_si: HEN1
AGGGG	HOCOMOCO v9	9.5e-06	INSM1_f1: INSM1
	JASPAR 2014	1.6e-05	MA0057: MZF1_5-13
	HumanTF 1.0	1.9e-05	NFKB1_DBDB: NFKB1
	HumanTF 1.0	2.1e-05	NFKB2_DBDB: NFKB2
	JASPAR 2014	3.6e-05	MA0155: INSM1
	HOCOMOCO v9	3.9e-05	ZN148_si: ZN148

	JASPAR 2014	4.9e-05	MA0163: PLAG1
	HOCOMOCO v9	4.9e-05	PLAG1_f1: PLAG1
	HOCOMOCO v9	5.0e-05	ZN219_f1: ZN219
	HumanTF 1.0	1.3e-04	KLF13_full: KLF13
ATACG	HOCOMOCO v9	1.7e-05	EOMES_f1: EOMES
	3D-footprint	3.5e-05	2jpa_A: Wilms tumor 1
	JASPAR 2014	0.001	MA0124: NKX3-1
	HumanTF 1.0	0.002	GMEB2_DBDB_1: GMEB2
	3D-footprint	0.005	1mhd_AB: SMAD3
	3D-footprint	0.006	2c6y_AB: FORKHEAD BOX PROTEIN K2
	HumanTF 1.0	0.006	GCM1_full_1: GCM1
	HumanTF 1.0	0.006	HOXC12_DBDB_2: HOXC12
	HumanTF 1.0	0.006	HOXD12_DBDB_2: HOXD12
	HumanTF 1.0	0.007	HOXC13_DBDB_2: HOXC13
	HOCOMOCO v9	1.7e-05	EOMES_f1: EOMES
	3D-footprint	3.5e-05	2jpa_A: Wilms tumor 1
	JASPAR 2014	0.001	MA0124: NKX3-1
ATACG	HumanTF 1.0	0.002	GMEB2_DBDB_1: GMEB2
	3D-footprint	0.005	1mhd_AB: SMAD3
	3D-footprint	0.006	2c6y_AB: FORKHEAD BOX PROTEIN K2
	HumanTF 1.0	0.006	GCM1_full_1: GCM1
	HumanTF 1.0	0.006	HOXC12_DBDB_2: HOXC12
	HumanTF 1.0	0.006	HOXD12_DBDB_2: HOXD12
	HumanTF 1.0	0.007	HOXC13_DBDB_2: HOXC13
	3D-footprint	1.2e-07	2e42_A: CCAAT/enhancer-binding protein beta
	3D-footprint	1.8e-06	1gu4_AB: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	1.8e-06	2e43_AB: CCAAT/enhancer-binding protein beta
	3D-footprint	3.7e-06	1gtw_AB: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	4.7e-06	2e42_AB: CCAAT/enhancer-binding protein beta
TTGCG	HumanTF 1.0	5.9e-06	CEBPG_full: CEBPG
	HumanTF 1.0	5.9e-06	CEBPG_DBDB: CEBPG
	HOCOMOCO v9	6.3e-06	AHR_si: AHR
	HumanTF 1.0	6.5e-06	CEBPD_DBDB: CEBPD
	HumanTF 1.0	6.7e-06	CEBPB_DBDB: CEBPB
	HumanTF 1.0	1.5e-05	HOMEZ_DBDB: HOMEZ
	HumanTF 1.0	5.1e-05	IRF9_full: IRF9
	HumanTF 1.0	1.1e-04	VENTX_DBDB_2: VENTX
	HumanTF 1.0	1.3e-04	IRF7_DBDB_2: IRF7
	HumanTF 1.0	5.5e-04	CENPB_full: CENPB
	HOCOMOCO v9	0.001	STAT2_f1: STAT2
	HumanTF 1.0	0.003	VENTX_DBDB_1: VENTX
	3D-footprint	0.004	2a07_IK: Forkhead box protein P2

	HumanTF 1.0	0.004	HSFY2_DBDB_2: HSFY2
	HumanTF 1.0	0.004	HOXC11_DBDB_1: HOXC11
CCGTT	HumanTF 1.0	9.8e-06	MYBL2_DBDB_3: MYBL2
	HumanTF 1.0	1.2e-05	MYBL1_DBDB_3: MYBL1
	HumanTF 1.0	1.5e-05	MYBL1_DBDB_2: MYBL1
	HumanTF 1.0	2.7e-05	MYBL1_DBDB_1: MYBL1
	HumanTF 1.0	3.1e-05	MYBL2_DBDB_4: MYBL2
	HumanTF 1.0	3.5e-05	MYBL2_DBDB_2: MYBL2
	3D-footprint	4.8e-05	1h89_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.7e-05	1h8a_ABC: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	7.8e-05	1h88_ABC: CCAAT/ENHANCER BINDING PROTEIN BETA
	HumanTF 1.0	9.3e-05	BARHL2_full_1: BARHL2
TCGGC	3D-footprint	0.001	4eot_A: Transcription factor MafA
	3D-footprint	0.003	1srs_B: PROTEIN (SERUM RESPONSE FACTOR (SRF))
	HOCOMOCO v9	0.003	NFIA+NFIB+NFIC+NFIX_si: NFIA+NFIB+NFIC+NFIX
	JASPAR 2014	0.005	MA0161: NFIC
	HOCOMOCO v9	0.005	MAFK_si: MAFK
	HumanTF 1.0	0.006	IRF5_full_2: IRF5
	HOCOMOCO v9	0.006	MAF_f1: MAF
	HOCOMOCO v9	0.006	TYY1_f2: TYY1
	3D-footprint	0.009	4is1_C: Zinc finger protein 217
	HOCOMOCO v9	0.009	PAX5_si: PAX5
GGCGG	HOCOMOCO v9	8.8e-06	SP1_f1: SP1
	HOCOMOCO v9	9.6e-06	EGR1_f2: EGR1
	HumanTF 1.0	1.1e-05	YY2_full: YY2
	HOCOMOCO v9	1.2e-05	E2F6_f1: E2F6
	HOCOMOCO v9	1.2e-05	TYY1_f2: TYY1
	HOCOMOCO v9	1.2e-05	EGR2_si: EGR2
	HumanTF 1.0	1.2e-05	YY2_DBDB: YY2
	HumanTF 1.0	1.4e-05	E2F8_DBDB: E2F8
	JASPAR 2014	1.8e-05	MA0471: E2F6
	HOCOMOCO v9	1.9e-05	KLF6_si: KLF6
TCGTG	HumanTF 1.0	2.6e-05	FOXO6_DBDB_3: FOXO6
	HumanTF 1.0	3.4e-05	GLIS3_DBDB: GLIS3
	HumanTF 1.0	3.6e-05	ZNF713_full: ZNF713
	HumanTF 1.0	5.3e-05	GLIS1_DBDB: GLIS1
	HOCOMOCO v9	7.6e-05	HES1_f1: HES1
	HumanTF 1.0	8.6e-05	ZNF282_DBDB: ZNF282
	3D-footprint	1.3e-04	1nkp_E: Max protein
	3D-footprint	1.3e-04	1nlw_D: MAD PROTEIN

	3D-footprint	1.3e-04	1an2_A: PROTEIN (TRANSCRIPTION FACTOR MAX (TF MAX))
	3D-footprint	1.4e-04	1nkp_A: Myc proto-oncogene protein
GCGTC	HOCOMOCO v9	1.7e-04	ATF3_f1: ATF3
	3D-footprint	1.8e-04	1jnm_B: PROTO-ONCOGENE C-JUN
	HOCOMOCO v9	2.2e-04	HEN1_si: HEN1
	HumanTF 1.0	2.7e-04	PROX1_DB: PROX1
	HumanTF 1.0	8.4e-04	ATF4_DB: ATF4
	HumanTF 1.0	9.3e-04	HINFP1_full_1: HINFP1
	HOCOMOCO v9	0.002	CREB1_f1: CREB1
	JASPAR 2014	0.002	MA0018: CREB1
	3D-footprint	0.002	1jnm_AB: PROTO-ONCOGENE C-JUN
	HOCOMOCO v9	0.002	AHR_si: AHR
CCGGT	HOCOMOCO v9	6.0e-06	ELK4_f1: ELK4
	HumanTF 1.0	6.0e-06	GRHL1_DB: GRHL1
	HumanTF 1.0	6.1e-06	ELK1_full_1: ELK1
	HumanTF 1.0	6.1e-06	FLI1_full_1: FLI1
	HumanTF 1.0	6.3e-06	ETV3_DB: ETV3
	HumanTF 1.0	6.5e-06	ETS1_full_1: ETS1
	HumanTF 1.0	6.6e-06	ERG_full_1: ERG
	HumanTF 1.0	6.6e-06	ELK4_DB: ELK4
	HumanTF 1.0	6.8e-06	ELK1_DB: ELK1
	HumanTF 1.0	6.9e-06	FEV_DB: FEV
ACCCA	HOCOMOCO v9	6.2e-06	GLI3_si: GLI3
	HOCOMOCO v9	6.6e-06	GLI2_f1: GLI2
	HOCOMOCO v9	6.7e-06	GLI1_f1: GLI1
	HumanTF 1.0	5.7e-05	GLI2_DB: GLI2
	HOCOMOCO v9	1.1e-04	BRCA1_f1: BRCA1
	3D-footprint	1.3e-04	2o61_B: Nuclear factor NF-kappa-B p105 subunit
	HOCOMOCO v9	1.6e-04	EGR3_f1: EGR3
	HOCOMOCO v9	1.7e-04	KLF3_f1: KLF3
	HumanTF 1.0	1.8e-04	ZNF143_DB: ZNF143
	HOCOMOCO v9	2.1e-04	ZN423_f1: ZN423
CGCTC	3D-footprint	0.006	1cf7_AB: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	3D-footprint	0.007	1cf7_A: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HOCOMOCO v9	0.007	ZBTB6_si: ZBTB6
	HumanTF 1.0	0.008	HOXD13_DB: HOXD13
	HumanTF 1.0	0.010	HOXC13_DB: HOXC13
CGCTT	HOCOMOCO v9	3.6e-05	IRF9_f1: IRF9
	HumanTF 1.0	4.3e-05	SPI1_full: SPI1
	HOCOMOCO v9	5.1e-05	TCF7_f1: TCF7
	HOCOMOCO v9	9.9e-05	SOX4_f1: SOX4

	HOCOMOCO v9	1.1e-04	PAX6_f1: PAX6
	HumanTF 1.0	1.3e-04	SPIB_DBDB: SPIB
	HumanTF 1.0	2.5e-04	IRF7_DBDB_1: IRF7
	HumanTF 1.0	2.6e-04	ETV6_full_1: ETV6
	HOCOMOCO v9	3.4e-04	IRF3_f1: IRF3
	HumanTF 1.0	4.2e-04	PAX2_DBDB: PAX2
ACGTA	HumanTF 1.0	1.3e-05	GMEB2_DBDB_1: GMEB2
	HOCOMOCO v9	1.6e-05	HIF1A_si: HIF1A
	HumanTF 1.0	1.9e-05	DBP_DBDB: DBP
	HumanTF 1.0	3.3e-05	GMEB2_DBDB_3: GMEB2
	HumanTF 1.0	5.3e-05	TEF_DBDB: TEF
	HumanTF 1.0	5.3e-05	DBP_full: DBP
	HumanTF 1.0	6.0e-05	GMEB2_DBDB_2: GMEB2
	HOCOMOCO v9	1.2e-04	E4F1_f1: E4F1
	JASPAR 2014	2.1e-04	MA0030: FOXF2
	HumanTF 1.0	3.2e-04	HLF_full: HLF
GCGCT	HOCOMOCO v9	7.7e-05	TCF7_f1: TCF7
	HumanTF 1.0	2.8e-04	CTCF_full: CTCF
	HOCOMOCO v9	3.6e-04	REST_f1: REST
	JASPAR 2014	6.2e-04	MA0138: REST
	3D-footprint	0.001	1cf7_AB: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	3D-footprint	0.001	1cf7_A: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	3D-footprint	0.002	2e43_AB: CCAAT/enhancer-binding protein beta
	3D-footprint	0.003	1gtw_AB: CAAT/ENHANCER BINDING PROTEIN BETA
	HOCOMOCO v9	0.003	E2F5_do: E2F5
	HumanTF 1.0	0.003	LHX6_full_2: LHX6
TCGAT	HumanTF 1.0	1.2e-05	CUX2_DBDB_2: CUX2
	HumanTF 1.0	1.6e-05	PAX7_full: PAX7
	HumanTF 1.0	2.3e-05	CUX1_DBDB_3: CUX1
	HumanTF 1.0	4.4e-05	PAX3_DBDB: PAX3
	HumanTF 1.0	4.6e-05	CUX2_DBDB_1: CUX2
	HOCOMOCO v9	5.6e-05	CUX1_f1: CUX1
	HumanTF 1.0	7.6e-05	ONECUT1_full: ONECUT1
	HumanTF 1.0	8.0e-05	ONECUT2_DBDB: ONECUT2
	HumanTF 1.0	8.3e-05	CUX1_DBDB_1: CUX1
	HumanTF 1.0	8.5e-05	CUX1_DBDB_2: CUX1
TAGTT	HumanTF 1.0	1.5e-04	IRF4_full: IRF4
	HOCOMOCO v9	3.9e-04	RORA_f1: RORA
	HumanTF 1.0	4.0e-04	IRF5_full_2: IRF5
	HOCOMOCO v9	6.9e-04	MYB_f1: MYB
	HumanTF 1.0	0.002	RORA_DBDB_2: RORA

	HOCOMOCO v9	0.002	DLX2_f1: DLX2
	HOCOMOCO v9	0.002	NR1I2_si: NR1I2
	HumanTF 1.0	0.002	EMX1_DBDB_2: EMX1
	HumanTF 1.0	0.002	RARA_full_3: RARA
	3D-footprint	0.002	2a07_IK: Forkhead box protein P2
GCGGC	HOCOMOCO v9	1.2e-05	TYY1_f2: TYY1
	JASPAR 2014	5.9e-05	MA0095: YY1
	HOCOMOCO v9	1.6e-04	EGR4_f1: EGR4
	HumanTF 1.0	5.3e-04	YY1_full: YY1
	3D-footprint	0.001	1h9d_C: CORE-BINDING FACTOR ALPHA SUBUNIT1
	3D-footprint	0.002	1gtw_B: CAAT/ENHANCER BINDING PROTEIN BETA
	3D-footprint	0.002	1h88_B: CCAAT/ENHANCER BINDING PROTEIN BETA
	HOCOMOCO v9	0.003	HESX1_f1: HESX1
	HumanTF 1.0	0.004	RUNX2_DBDB_3: RUNX2
TCGCC	HumanTF 1.0	0.004	GCM2_DBDB: GCM2
	HumanTF 1.0	2.7e-05	ZBTB7A_DBDB: ZBTB7A
	3D-footprint	4.1e-05	1ic8_B: HEPATOCYTE NUCLEAR FACTOR 1-ALPHA
	3D-footprint	1.3e-04	1cf7_B: PROTEIN (TRANSCRIPTION FACTOR DP-2)
	3D-footprint	4.9e-04	1am9_A: PROTEIN (STEROL REGULATORY ELEMENT BINDING PROTEIN 1A)
	HumanTF 1.0	6.2e-04	ZBTB49_DBDB: ZBTB49
	3D-footprint	0.001	1cf7_AB: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	3D-footprint	0.001	1cf7_A: PROTEIN (TRANSCRIPTION FACTOR E2F-4)
	HOCOMOCO v9	0.002	TAL1_f2: TAL1
	HumanTF 1.0	0.002	FOXB1_DBDB_1: FOXB1
	3D-footprint	0.003	1a3q_A: PROTEIN (NUCLEAR FACTOR KAPPA-B P52)
TCCAG	HumanTF 1.0	2.2e-05	ZNF238_DBDB: ZNF238
	HumanTF 1.0	3.1e-05	ZNF238_full: ZNF238
	HOCOMOCO v9	4.3e-05	STAT3_si: STAT3
	3D-footprint	1.3e-04	3cbb_A: Hepatocyte Nuclear Factor 4-alpha, DNA binding domain
	3D-footprint	1.4e-04	1pzu_B: Nuclear factor of activated T-cells, cytoplasmic 2
	3D-footprint	1.4e-04	1imh_C: NUCLEAR FACTOR OF ACTIVATED T CELLS 5
	3D-footprint	3.5e-04	1k6o_B: Serum response factor
	JASPAR 2014	4.4e-04	MA0130: ZNF354C
	JASPAR 2014	5.3e-04	MA0114: HNF4A
	HOCOMOCO v9	6.0e-04	STA5A_do: STA5A
CTGGG	HOCOMOCO v9	1.1e-05	TWST1_f1: TWST1

	HOCOMOCO v9	2.6e-05	COE1_f2: COE1
	HOCOMOCO v9	4.9e-05	STAT4_si: STAT4
	HOCOMOCO v9	7.9e-05	AP2C_f1: AP2C
	HOCOMOCO v9	1.2e-04	AP2A_f2: AP2A
	JASPAR 2014	1.2e-04	MA0144: STAT3
	JASPAR 2014	1.3e-04	MA0154: EBF1
	3D-footprint	1.3e-04	2o61_B: Nuclear factor NF-kappa-B p105 subunit
	JASPAR 2014	3.7e-04	MA0524: TFAP2C
	HOCOMOCO v9	5.2e-04	STAT6_do: STAT6
TTAGT	3D-footprint	3.7e-06	2me6_A: Homeobox protein GBX-1
	3D-footprint	3.1e-05	1srs_AB: PROTEIN (SERUM RESPONSE FACTOR (SRF))
	3D-footprint	8.7e-05	1hbx_ABG: SERUM RESPONSE FACTOR
	HumanTF 1.0	9.7e-05	LHX6_full_1: LHX6
	HumanTF 1.0	2.1e-04	LHX2_DB1: LHX2
	HumanTF 1.0	3.0e-04	GSX2_DB1: GSX2
	3D-footprint	3.6e-04	1srs_B: PROTEIN (SERUM RESPONSE FACTOR (SRF))
	HumanTF 1.0	5.0e-04	HOXB5_DB1: HOXB5
	HumanTF 1.0	7.2e-04	ESX1_full: ESX1
	JASPAR 2014	8.6e-04	MA0158: HOXA5
ATTAT	3D-footprint	1.3e-07	3cmy_A: Paired box protein Pax-3
	HOCOMOCO v9	3.9e-06	ZN333_f1: ZN333
	HOCOMOCO v9	5.8e-06	DLX2_f1: DLX2
	HumanTF 1.0	1.2e-05	DPRX_DB1: DPRX
	HumanTF 1.0	1.3e-05	DLX1_DB1: DLX1
	HumanTF 1.0	2.0e-05	RHOXF1_DB1: RHOXF1
	3D-footprint	3.3e-05	2h8r_AB: Hepatocyte nuclear factor 1-beta
	HumanTF 1.0	3.6e-05	ZNF410_DB1: ZNF410
	HumanTF 1.0	4.4e-05	POU4F2_full: POU4F2
	3D-footprint	4.8e-05	1ic8_AB: HEPATOCYTE NUCLEAR FACTOR 1-ALPHA
ATTCT	3D-footprint	1.6e-06	3uk3_D: Zinc finger protein 217
	3D-footprint	4.4e-05	3uk3_CD: Zinc finger protein 217
	3D-footprint	4.4e-05	4is1_CD: Zinc finger protein 217
	JASPAR 2014	2.5e-04	MA0036: GATA2
	3D-footprint	0.001	4is1_C: Zinc finger protein 217
	HumanTF 1.0	0.002	HSF1_full: HSF1
	HumanTF 1.0	0.002	TEAD3_DB1: TEAD3
	JASPAR 2014	0.003	MA0113: NR3C1
	HOCOMOCO v9	0.003	HSF2_si: HSF2
	3D-footprint	0.003	3ri4_D: Protein C-ets-1
GATAG	HumanTF 1.0	6.7e-05	ZBED1_DB1: ZBED1
	HOCOMOCO v9	1.6e-04	GATA3_si: GATA3

HOCOMOCO v9	2.0e-04	ZBTB6_si: ZBTB6
3D-footprint	4.0e-04	1puf_B: Pre-B-cell leukemia transcription factor-1
HOCOMOCO v9	6.1e-04	GATA6_f2: GATA6
HOCOMOCO v9	0.001	GATA2_si: GATA2
JASPAR 2014	0.002	MA0037: GATA3
HOCOMOCO v9	0.002	GATA4_f1: GATA4
HumanTF 1.0	0.002	GATA3_DB: GATA3
HumanTF 1.0	0.002	GATA3_full: GATA3

Legend: **Motif** - motif sequence associatef with TF-binding. **Source** – the name of database where the association of the motif with the transcription factor was identified. **E-value** – the expect value, a parameter that describes the number of hits one can "expect" to see by chance when searching a database of a particular size. **Protein** – the name of a protein (transcription factor) associated with the motif.

Supplementary table 10. 66 DEG-associated transcription factors identified both by cisExpress and MetaCore and not identified in Swindell, Sarkar (20).

Ensembl Gene ID	Gene symbol	Transcription factor name
ENSG00000106546	AHR	aryl hydrocarbon receptor
ENSG00000169083	AR	androgen receptor
ENSG00000133794	ARNTL	aryl hydrocarbon receptor nuclear translocator-like
ENSG00000115966	ATF2	activating transcription factor 2
ENSG00000162772	ATF3	activating transcription factor 3
ENSG00000128272	ATF4	activating transcription factor 4 (tax-responsive enhancer element B67); activating transcription factor 4C
ENSG00000128272	ATF4C	activating transcription factor 4 (tax-responsive enhancer element B67); activating transcription factor 4C
ENSG00000184771	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha
ENSG00000172216	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta
ENSG00000221869	CEBD	CCAAT/enhancer binding protein (C/EBP), delta
ENSG00000092067	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon
ENSG00000095794	CREM	cAMP responsive element modulator
ENSG00000007968	E2F2	E2F transcription factor 2
ENSG00000112242	E2F3	E2F transcription factor 3
ENSG00000205250	E2F4	E2F transcription factor 4, p107/p130-binding
ENSG00000133740	E2F5	E2F transcription factor 5, p130-binding
ENSG00000129173	E2F8	E2F transcription factor 8
ENSG00000122877	EGR2	early growth response 2
ENSG00000179388	EGR3	early growth response 3
ENSG00000163435	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)
ENSG00000091831	ESR1	estrogen receptor 1
ENSG00000119715	ESRRB	estrogen-related receptor beta
ENSG00000157557	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
ENSG00000175832	ETV4	ets variant 4
ENSG00000129514	FOXA1	forkhead box A1
ENSG00000154727	GABPA	GA binding protein transcription factor, alpha subunit 60kDa
ENSG00000074047	GLI2	GLI family zinc finger 2
ENSG00000100644	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
ENSG00000185122	HSF1	heat shock transcription factor 1

ENSG00000168310	IRF2	interferon regulatory factor 2
ENSG00000126456	IRF3	interferon regulatory factor 3
ENSG00000137265	IRF4	interferon regulatory factor 4
ENSG00000128604	IRF5	interferon regulatory factor 5
ENSG00000185507	IRF7	interferon regulatory factor 7
ENSG00000140968	IRF8	interferon regulatory factor 8
ENSG00000067082	KLF6	Kruppel-like factor 6
ENSG00000138795	LEF1	lymphoid enhancer-binding factor 1
ENSG00000198517	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)
ENSG00000118513	MYB	v-myb myeloblastosis viral oncogene homolog (avian)
ENSG00000101057	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
ENSG00000131196	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
ENSG00000123405	NFE2	nuclear factor (erythroid-derived 2), 45kDa
ENSG00000141905	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)
ENSG00000001167	NFYA	nuclear transcription factor Y, alpha
ENSG00000144852	NR1I2	nuclear receptor subfamily 1, group I, member 2
ENSG00000143257	NR1I3	nuclear receptor subfamily 1, group I, member 3
ENSG00000116833	NR5A2	nuclear receptor subfamily 5, group A, member 2
ENSG00000196092	PAX5	paired box 5
ENSG00000186951	PPARA	peroxisome proliferator-activated receptor alpha
ENSG00000132170	PPARG	peroxisome proliferator-activated receptor gamma
ENSG00000110851	PRDM4	PR domain containing 4
ENSG00000117707	PROX1	prospero homeobox 1
ENSG00000069667	RORA	RAR-related orphan receptor A
ENSG00000124813	RUNX2	runt-related transcription factor 2
ENSG00000124216	SNAI1	snail homolog 1 (Drosophila)
ENSG00000185591	SP1	Sp1 transcription factor
ENSG00000172845	SP3	Sp3 transcription factor
ENSG00000198911	SREBF2	sterol regulatory element binding transcription factor 2
ENSG00000170581	STAT2	signal transducer and activator of transcription 2, 113kDa
ENSG00000168610	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)
ENSG00000138378	STAT4	signal transducer and activator of transcription 4
ENSG00000126561	STAT5A	signal transducer and activator of transcription 5A
ENSG0000008196	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
ENSG00000090447	TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)
ENSG00000198176	TFDP1	transcription factor Dp-1
ENSG00000158773	USF1	upstream transcription factor 1
ENSG00000166478	ZNF143	zinc finger protein 143

Supplementary table 11. Interleukins differentially expressed in psoriatic skin.

Ensembl_ID	Gene name	Fold Change	FDR	DEG
ENSG00000136694	<i>IL36A</i>	38.31	0.00	+
ENSG00000142224	<i>IL19</i>	16.59	0.00	+
ENSG00000169429	<i>IL8</i>	16.31	0.00	+
ENSG00000136688	<i>IL36G</i>	10.12	0.00	+
ENSG00000162891	<i>IL20</i>	8.63	0.00	+

ENSG00000125538	<i>IL1B</i>	6.50	0.00	+
ENSG00000112116	<i>IL17F</i>	4.54	0.00	+
ENSG00000136695	<i>IL36RN</i>	4.28	0.00	+
ENSG00000168685	<i>IL7R</i>	3.51	0.06	
ENSG00000112115	<i>IL17A</i>	3.29	0.00	+
ENSG00000111536	<i>IL26</i>	3.12	0.00	+
ENSG00000077238	<i>IL4R</i>	2.94	0.00	+
ENSG00000124391	<i>IL17C</i>	2.89	0.00	+
ENSG00000134460	<i>IL2RA</i>	2.82	0.00	+
ENSG00000127318	<i>IL22</i>	2.62	0.02	+
ENSG00000162892	<i>IL24</i>	2.44	0.01	+
ENSG00000147168	<i>IL2RG</i>	2.37	0.00	+
ENSG00000008517	<i>IL32</i>	2.25	0.00	+
ENSG00000110324	<i>IL10RA</i>	2.16	0.00	+
ENSG00000136689	<i>IL1RN</i>	2.16	0.00	+
ENSG00000115607	<i>IL18RAP</i>	2.00	0.05	
ENSG00000081985	<i>IL12RB2</i>	1.89	0.02	+
ENSG00000103522	<i>IL21R</i>	1.81	0.10	
ENSG00000110944	<i>IL23A</i>	1.74	0.26	
ENSG00000113302	<i>IL12B</i>	1.73	0.29	
ENSG00000100385	<i>IL2RB</i>	1.67	0.18	
ENSG00000137033	<i>IL33</i>	1.61	0.88	
ENSG00000131724	<i>IL13RA1</i>	1.61	0.21	
ENSG00000096996	<i>IL12RB1</i>	1.58	0.27	
ENSG00000115604	<i>IL18R1</i>	1.54	0.34	
ENSG00000115602	<i>IL1RL1</i>	1.54	0.34	
ENSG00000136696	<i>IL36B</i>	1.52	0.52	
ENSG00000115008	<i>IL1A</i>	1.41	1.00	
ENSG00000164136	<i>IL15</i>	1.40	0.70	
ENSG00000134470	<i>IL15RA</i>	1.36	0.78	
ENSG00000104951	<i>IL4I1</i>	1.35	0.82	
ENSG00000164485	<i>IL22RA2</i>	1.35	0.86	
ENSG00000104998	<i>IL27RA</i>	1.34	0.70	
ENSG00000136634	<i>IL10</i>	1.34	0.79	
ENSG00000227145	<i>IL21-ASI</i>	1.32	1.00	
ENSG00000196083	<i>IL1RAP</i>	1.31	1.00	
ENSG00000142677	<i>IL22RA1</i>	1.25	1.00	
ENSG00000188263	<i>IL17REL</i>	1.24	1.00	
ENSG00000138684	<i>IL21</i>	1.20	1.00	
ENSG00000243646	<i>IL10RB</i>	1.18	1.00	
ENSG00000115594	<i>IL1R1</i>	1.18	1.00	
ENSG00000223799	<i>IL10RB-ASI</i>	1.17	1.00	
ENSG00000169194	<i>IL13</i>	1.16	1.00	

ENSG00000197272	<i>IL27</i>	1.11	1.00	
ENSG00000113525	<i>IL5</i>	1.09	1.00	
ENSG00000136244	<i>IL6</i>	1.09	1.00	
ENSG00000177663	<i>IL17RA</i>	1.08	1.00	
ENSG00000166090	<i>IL25</i>	1.08	1.00	
ENSG00000160712	<i>IL6R</i>	1.07	1.00	
ENSG00000115590	<i>IL1R2</i>	1.06	1.00	
ENSG00000172349	<i>IL16</i>	1.04	1.00	
ENSG00000227018	<i>IL6STP1</i>	1.04	1.00	
ENSG00000134352	<i>IL6ST</i>	1.03	1.00	
ENSG00000115598	<i>IL1RL2</i>	1.02	1.00	
ENSG00000091181	<i>IL5RA</i>	1.01	1.00	
ENSG00000113520	<i>IL4</i>	1.01	1.00	
ENSG00000189108	<i>IL1RAPL2</i>	1.00	1.00	
ENSG00000172458	<i>IL17D</i>	1.00	1.00	
ENSG00000162594	<i>IL23R</i>	1.00	1.00	
ENSG00000234910	<i>IL6RP1</i>	0.98	1.00	
ENSG00000164399	<i>IL3</i>	0.97	1.00	
ENSG00000095752	<i>IL11</i>	0.95	1.00	
ENSG00000204671	<i>IL31</i>	0.94	1.00	
ENSG00000169306	<i>IL1RAPL1</i>	0.93	1.00	
ENSG00000124334	<i>IL9R</i>	0.92	1.00	
ENSG00000104432	<i>IL7</i>	0.92	1.00	
ENSG00000145839	<i>IL9</i>	0.90	1.00	
ENSG00000123496	<i>IL13RA2</i>	0.89	1.00	
ENSG00000109471	<i>IL2</i>	0.85	1.00	
ENSG00000137496	<i>IL18BP</i>	0.85	1.00	
ENSG00000168811	<i>IL12A</i>	0.85	1.00	
ENSG00000174564	<i>IL20RB</i>	0.83	1.00	
ENSG00000249407	<i>IL20RB-ASI</i>	0.83	1.00	
ENSG00000144730	<i>IL17RD</i>	0.83	1.00	
ENSG00000136697	<i>IL1F10</i>	0.82	1.00	
ENSG00000164509	<i>IL31RA</i>	0.81	1.00	
ENSG00000137070	<i>IL11RA</i>	0.75	0.93	
ENSG00000150782	<i>IL18</i>	0.74	0.62	
ENSG00000185291	<i>IL3RA</i>	0.71	0.97	
ENSG00000056736	<i>IL17RB</i>	0.70	0.70	
ENSG00000016402	<i>IL20RA</i>	0.66	0.51	
ENSG00000163702	<i>IL17RC</i>	0.64	0.38	
ENSG00000127743	<i>IL17B</i>	0.64	0.51	
ENSG00000163701	<i>IL17RE</i>	0.52	0.02	+
ENSG00000157368	<i>IL34</i>	0.26	0.00	+
ENSG00000125571	<i>IL37</i>	0.20	0.00	+

Legend: Ensembl_ID – ID according to Ensembl database; Gene name - official gene symbol; FC – fold change of gene expression in lesional versus non-lesional psoriatic skin; FDR – p-value, corrected for multiple comparisons. Bold “Gene name” and “+” in the “DEG” column indicates significant differential gene expression. Zero values for paired p-value and FDR are used for the numbers less than 10^{-16} .

Supplementary table 12. FOXA1-target genes, identified as differentially expressed in present analysis.

Ensembl_ID	Gene name	Fold Change	FDR
ENSG00000143546	<i>S100A8</i>	27.643	0.000
ENSG00000163220	<i>S100A9</i>	23.819	0.000
ENSG00000163739	<i>CXCL1</i>	23.744	0.000
ENSG00000163221	<i>S100A12</i>	23.225	0.000
ENSG00000153802	<i>TMPRSS11D</i>	22.691	0.000
ENSG00000135114	<i>OASL</i>	17.261	0.021
ENSG00000170465	<i>KRT6C</i>	14.057	0.004
ENSG00000148346	<i>LCN2</i>	11.796	0.000
ENSG00000165474	<i>GJB2</i>	11.552	0.000
ENSG00000104368	<i>PLAT</i>	9.420	0.000
ENSG00000172382	<i>PRSS27</i>	8.474	0.000
ENSG00000185479	<i>KRT6B</i>	7.954	0.000
ENSG00000183696	<i>UPP1</i>	7.856	0.000
ENSG00000182585	<i>EPGN</i>	7.760	0.000
ENSG00000167755	<i>KLK6</i>	7.604	0.000
ENSG00000128965	<i>CHAC1</i>	6.702	0.000
ENSG00000205021	<i>CCL3L1</i>	6.062	0.000
ENSG00000169174	<i>PCSK9</i>	5.900	0.000
ENSG00000196136	<i>SERPINA3</i>	5.577	0.000
ENSG00000197262	<i>CCL4L2</i>	4.873	0.000
ENSG00000171124	<i>FUT3</i>	4.687	0.000
ENSG00000064886	<i>CHI3L2</i>	4.535	0.000
ENSG00000183347	<i>GBP6</i>	4.484	0.000
ENSG00000145113	<i>MUC4</i>	4.463	0.000
ENSG00000197249	<i>SERPINA1</i>	4.335	0.000
ENSG00000174502	<i>SLC26A9</i>	4.076	0.000
ENSG00000131126	<i>TEX101</i>	3.815	0.000
ENSG00000124875	<i>CXCL6</i>	3.754	0.002
ENSG00000158125	<i>XDH</i>	3.647	0.003
ENSG00000118322	<i>ATP10B</i>	3.583	0.000
ENSG00000126353	<i>CCR7</i>	3.548	0.000
ENSG00000228211	<i>HYALP1</i>	3.517	0.000
ENSG00000179477	<i>ALOX12B</i>	3.489	0.000
ENSG00000182866	<i>LCK</i>	3.384	0.000

ENSG0000166278	<i>C2</i>	3.376	0.000
ENSG0000243649	<i>CFB</i>	3.376	0.000
ENSG0000151790	<i>TDO2</i>	3.357	0.000
ENSG0000125780	<i>TGM3</i>	3.355	0.030
ENSG0000186818	<i>LILRB4</i>	3.296	0.000
ENSG0000115267	<i>IFIH1</i>	3.274	0.000
ENSG0000077984	<i>CST7</i>	3.258	0.000
ENSG0000163218	<i>PGLYRP4</i>	3.224	0.000
ENSG0000153048	<i>CARHSP1</i>	3.203	0.000
ENSG0000111536	<i>IL26</i>	3.121	0.000
ENSG0000140105	<i>WARS</i>	3.110	0.000
ENSG0000183908	<i>LRRC55</i>	3.080	0.000
ENSG0000157193	<i>LRP8</i>	2.837	0.015
ENSG0000167618	<i>LAIR2</i>	2.826	0.006
ENSG0000134460	<i>IL2RA</i>	2.819	0.000
ENSG0000169129	<i>AFAP1L2</i>	2.798	0.000
ENSG0000163993	<i>S100P</i>	2.748	0.006
ENSG0000121552	<i>CSTA</i>	2.692	0.000
ENSG0000131042	<i>LILRB2</i>	2.635	0.000
ENSG0000242515	<i>UGT1A10</i>	2.633	0.000
ENSG0000196743	<i>GM2A</i>	2.604	0.000
ENSG0000163687	<i>DNASE1L3</i>	2.589	0.000
ENSG0000126787	<i>DLGAP5</i>	2.575	0.000
ENSG0000108691	<i>CCL2</i>	2.543	0.000
ENSG0000100368	<i>CSF2RB</i>	2.532	0.038
ENSG0000185338	<i>SOCS1</i>	2.511	0.003
ENSG0000108679	<i>LGALS3BP</i>	2.508	0.045
ENSG0000103222	<i>ABCC1</i>	2.488	0.000
ENSG0000064932	<i>SBNO2</i>	2.470	0.001
ENSG0000172575	<i>RASGRPI</i>	2.434	0.028
ENSG0000119535	<i>CSF3R</i>	2.416	0.027
ENSG0000134070	<i>IRAK2</i>	2.414	0.000
ENSG0000085831	<i>TTC39A</i>	2.408	0.000
ENSG0000171310	<i>CHST11</i>	2.403	0.019
ENSG0000187474	<i>FPR3</i>	2.393	0.028
ENSG0000136286	<i>MYO1G</i>	2.357	0.001
ENSG0000165181	<i>C9orf84</i>	2.294	0.002
ENSG0000170312	<i>CDK1</i>	2.239	0.001
ENSG0000132965	<i>ALOX5AP</i>	2.232	0.003
ENSG0000105122	<i>RASAL3</i>	2.218	0.005
ENSG0000211448	<i>DIO2</i>	2.197	0.014
ENSG0000165389	<i>SPTSSA</i>	2.191	0.003
ENSG0000148680	<i>HTR7</i>	2.186	0.020

ENSG0000125347	<i>IRF1</i>	2.177	0.003
ENSG0000157551	<i>KCNJ15</i>	2.176	0.001
ENSG0000131747	<i>TOP2A</i>	2.175	0.013
ENSG0000150337	<i>FCGR1A</i>	2.159	0.020
ENSG0000196684	<i>HSH2D</i>	2.133	0.015
ENSG0000167772	<i>ANGPTL4</i>	2.073	0.001
ENSG0000141968	<i>VAV1</i>	2.070	0.016
ENSG0000223865	<i>HLA-DPB1</i>	2.060	0.008
ENSG0000112033	<i>PPARD</i>	2.044	0.009
ENSG0000168610	<i>STAT3</i>	2.034	0.008
ENSG0000160703	<i>NLRX1</i>	2.005	0.016
ENSG0000121858	<i>TNFSF10</i>	2.000	0.007
ENSG0000167895	<i>TMC8</i>	1.991	0.024
ENSG0000160185	<i>UBASH3A</i>	1.988	0.026
ENSG0000145934	<i>TENM2</i>	1.979	0.011
ENSG0000092929	<i>UNC13D</i>	1.972	0.028
ENSG0000130558	<i>OLFM1</i>	1.971	0.024
ENSG0000170469	<i>SPATA24</i>	1.955	0.021
ENSG0000088325	<i>TPX2</i>	1.949	0.019
ENSG0000105755	<i>ETHE1</i>	1.945	0.031
ENSG0000162645	<i>GBP2</i>	1.940	0.014
ENSG0000049249	<i>TNFRSF9</i>	1.936	0.048
ENSG0000149781	<i>FERMT3</i>	1.933	0.028
ENSG0000138964	<i>PARVG</i>	1.924	0.036
ENSG0000159527	<i>PGLYRP3</i>	1.918	0.025
ENSG0000034063	<i>UHRF1</i>	1.912	0.021
ENSG0000104611	<i>SH2D4A</i>	1.884	0.028
ENSG0000196954	<i>CASP4</i>	1.879	0.036
ENSG0000125430	<i>HS3ST3B1</i>	1.872	0.033
ENSG0000006432	<i>MAP3K9</i>	1.850	0.042
ENSG0000184792	<i>OSBP2</i>	1.847	0.040
ENSG0000101846	<i>STS</i>	1.827	0.010
ENSG0000154096	<i>THY1</i>	1.826	0.032
ENSG0000101347	<i>SAMHD1</i>	1.815	0.044
ENSG0000175832	<i>ETV4</i>	1.806	0.022
ENSG0000124380	<i>SNRNP27</i>	1.797	0.041
ENSG0000165025	<i>SYK</i>	1.785	0.045
ENSG0000167232	<i>ZNF91</i>	0.541	0.039
ENSG0000106078	<i>COBL</i>	0.540	0.037
ENSG0000147257	<i>GPC3</i>	0.539	0.034
ENSG0000185567	<i>AHNAK2</i>	0.533	0.025
ENSG0000151729	<i>SLC25A4</i>	0.528	0.044
ENSG0000162817	<i>C1orf115</i>	0.527	0.026

ENSG00000112796	<i>ENPP5</i>	0.521	0.031
ENSG00000042832	<i>TG</i>	0.519	0.026
ENSG00000180354	<i>C7orf41</i>	0.515	0.018
ENSG00000156219	<i>ART3</i>	0.513	0.045
ENSG00000137880	<i>GCHFR</i>	0.510	0.047
ENSG00000163083	<i>INHBB</i>	0.509	0.016
ENSG00000156042	<i>TTC18</i>	0.505	0.017
ENSG00000128849	<i>CGNL1</i>	0.493	0.007
ENSG00000013588	<i>GPRC5A</i>	0.490	0.015
ENSG00000124145	<i>SDC4</i>	0.489	0.008
ENSG00000167972	<i>ABCA3</i>	0.486	0.010
ENSG00000166415	<i>WDR72</i>	0.485	0.028
ENSG00000012171	<i>SEMA3B</i>	0.485	0.018
ENSG00000166546	<i>BEANI</i>	0.484	0.045
ENSG00000162545	<i>CAMK2N1</i>	0.477	0.006
ENSG00000163686	<i>ABHD6</i>	0.476	0.005
ENSG00000137726	<i>FXYD6</i>	0.476	0.008
ENSG00000076555	<i>ACACB</i>	0.467	0.004
ENSG00000150556	<i>LYPD6B</i>	0.463	0.003
ENSG00000103319	<i>EEF2K</i>	0.462	0.003
ENSG00000101333	<i>PLCB4</i>	0.461	0.003
ENSG00000117472	<i>TSPAN1</i>	0.459	0.021
ENSG00000160191	<i>PDE9A</i>	0.442	0.003
ENSG00000174514	<i>MFSD4</i>	0.439	0.001
ENSG00000137936	<i>BCAR3</i>	0.438	0.001
ENSG00000165125	<i>TRPV6</i>	0.430	0.002
ENSG00000163347	<i>CLDN1</i>	0.428	0.003
ENSG00000131730	<i>CKMT2</i>	0.423	0.001
ENSG00000177465	<i>ACOT4</i>	0.422	0.023
ENSG00000065371	<i>ROPN1</i>	0.420	0.030
ENSG00000010319	<i>SEMA3G</i>	0.420	0.000
ENSG00000116299	<i>KIAA1324</i>	0.419	0.001
ENSG00000165810	<i>BTNL9</i>	0.418	0.000
ENSG00000104490	<i>NCALD</i>	0.417	0.000
ENSG00000246223	<i>C14orf64</i>	0.398	0.000
ENSG00000141469	<i>SLC14A1</i>	0.389	0.000
ENSG00000168913	<i>ENHO</i>	0.383	0.000
ENSG00000117525	<i>F3</i>	0.380	0.000
ENSG00000141750	<i>STAC2</i>	0.373	0.007
ENSG00000039987	<i>BEST2</i>	0.362	0.001
ENSG0000009950	<i>MLXIPL</i>	0.359	0.001
ENSG00000174697	<i>LEP</i>	0.352	0.008
ENSG00000204033	<i>LRIT2</i>	0.351	0.003

ENSG00000105357	<i>MYH14</i>	0.347	0.009
ENSG00000181092	<i>ADIPOQ</i>	0.321	0.025
ENSG00000116039	<i>ATP6V1B1</i>	0.314	0.001
ENSG00000160868	<i>CYP3A4</i>	0.308	0.000
ENSG00000103740	<i>ACSBG1</i>	0.307	0.001
ENSG00000110484	<i>SCGB2A2</i>	0.290	0.000
ENSG00000159339	<i>PADI4</i>	0.290	0.001
ENSG00000149090	<i>PAMR1</i>	0.288	0.000
ENSG00000130595	<i>TNNT3</i>	0.273	0.010
ENSG00000170323	<i>FABP4</i>	0.266	0.000
ENSG00000166816	<i>LDHD</i>	0.249	0.000
ENSG00000144908	<i>ALDH1L1</i>	0.228	0.000
ENSG00000119673	<i>ACOT2</i>	0.227	0.010
ENSG00000159763	<i>PIP</i>	0.226	0.023
ENSG00000185640	<i>KRT79</i>	0.218	0.004
ENSG00000165269	<i>AQP7</i>	0.218	0.000
ENSG00000125571	<i>IL37</i>	0.202	0.000
ENSG00000175315	<i>CST6</i>	0.178	0.001
ENSG00000168671	<i>UGT3A2</i>	0.157	0.000
ENSG00000103089	<i>FA2H</i>	0.156	0.000
ENSG00000184227	<i>ACOT1</i>	0.130	0.008
ENSG00000221968	<i>FADS3</i>	0.129	0.010
ENSG00000119915	<i>ELOVL3</i>	0.065	0.004
ENSG00000184210	<i>DGAT2L6</i>	0.061	0.028
ENSG00000147160	<i>AWAT2</i>	0.057	0.000

Legend: Ensembl_ID – ID according to Ensembl database; Gene name – official gene symbol; FC – fold change of gene expression in lesional versus non-lesional psoriatic skin; FDR – p-value, corrected for multiple comparisons. Zero values for paired p-value and FDR are used for the numbers less than 10⁻⁴.

Supplementary table 13. Gene ontologies of FOXA1 targets, identified as DEGs in RNA-Seq analysis (p-value≤0,01).

GO pathway ID	Number of genes in the cascade	%	PValue
Ontologies enriched with upregulated DEGs			
GO:0006952~defense response	27	24,11	2,20E-13
GO:0006955~immune response	26	23,21	2,06E-11
GO:0006954~inflammatory response	18	16,07	2,13E-10
GO:0009611~response to wounding	21	18,75	1,47E-09
GO:0045087~innate immune response	9	8,04	8,09E-06
GO:0042330~taxis	9	8,04	2,38E-05
GO:0006935~chemotaxis	9	8,04	2,38E-05
GO:0019221~cytokine-mediated signaling pathway	6	5,36	1,65E-04

GO:0007610~behavior	13	11,61	1,73E-04
GO:0007626~locomotory behavior	9	8,04	9,52E-04
GO:0050856~regulation of T cell receptor signaling pathway	3	2,68	0,002
GO:0006928~cell motion	11	9,82	0,003
GO:0050854~regulation of antigen receptor-mediated signaling pathway	3	2,68	0,003
GO:0002253~activation of immune response	5	4,46	0,005
GO:0002526~acute inflammatory response	5	4,46	0,006
GO:0042981~regulation of apoptosis	14	12,5	0,006
GO:0043067~regulation of programmed cell death	14	12,5	0,007
GO:0010941~regulation of cell death	14	12,5	0,007
GO:0002684~positive regulation of immune system process	7	6,25	0,008
GO:0019370~leukotriene biosynthetic process	3	2,68	0,009
GO:0043450~alkene biosynthetic process	3	2,68	0,009
GO:0016052~carbohydrate catabolic process	5	4,46	0,009
GO:0009615~response to virus	5	4,46	0,009
GO:0045321~leukocyte activation	7	6,25	0,009
GO:0006026~aminoglycan catabolic process	3	2,68	0,010
GO:0010647~positive regulation of cell communication	8	7,14	0,010
GO:0006691~leukotriene metabolic process	3	2,68	0,011
GO:0006022~aminoglycan metabolic process	4	3,57	0,012
GO:0043449~cellular alkene metabolic process	3	2,68	0,012
GO:0007267~cell-cell signaling	11	9,82	0,013
GO:0048545~response to steroid hormone stimulus	6	5,36	0,013
GO:0042110~T cell activation	5	4,46	0,014
GO:0009617~response to bacterium	6	5,36	0,014
GO:0043065~positive regulation of apoptosis	9	8,04	0,014

Ontologies enriched with downregulated DEGs

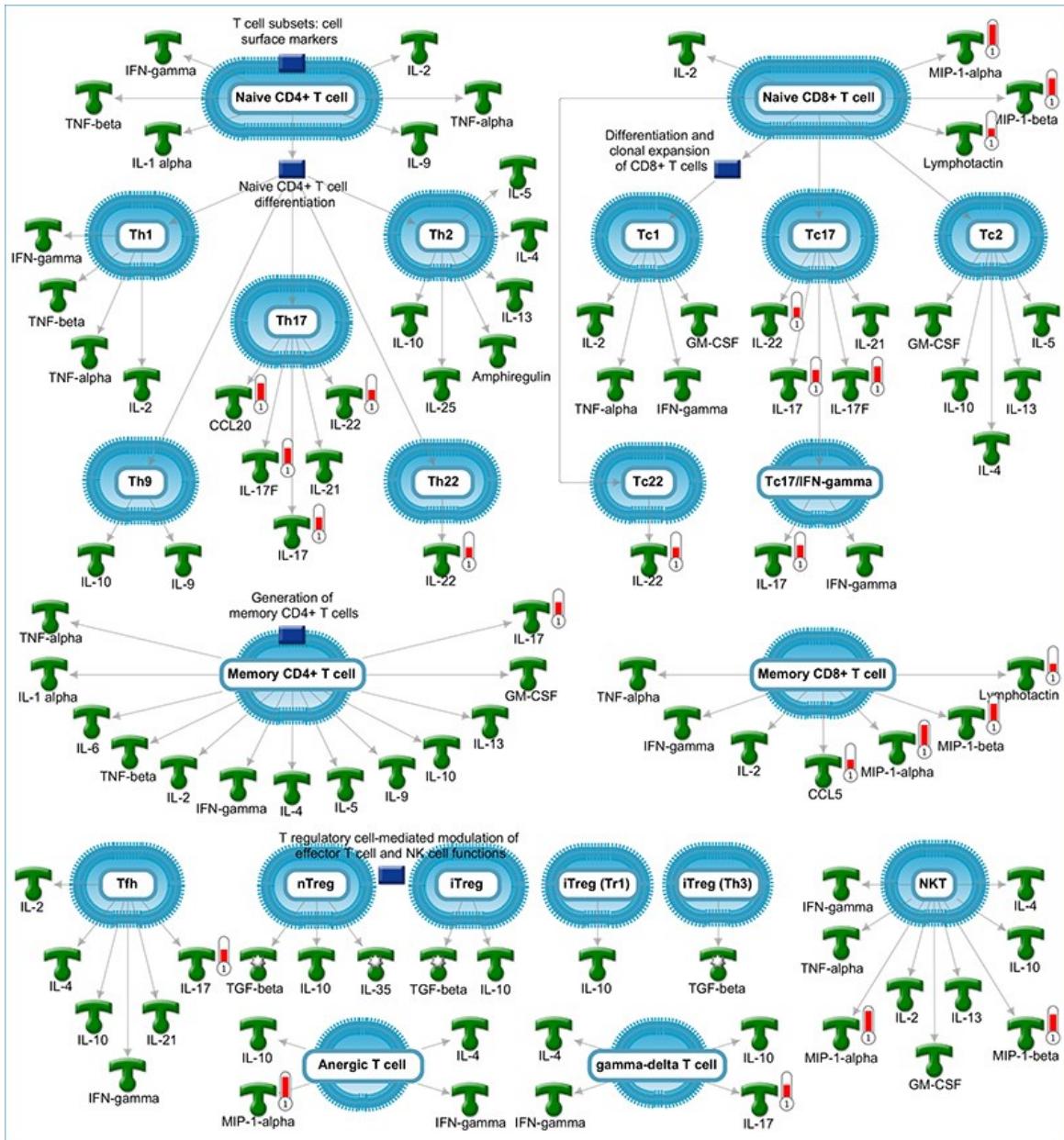
GO:0006631~fatty acid metabolic process	12	16,67	8,97E-11
GO:0001676~long-chain fatty acid metabolic process	4	5,56	1,55E-06
GO:0000038~very-long-chain fatty acid metabolic process	4	5,56	4,15E-05
GO:0006633~fatty acid biosynthetic process	5	6,94	1,87E-04
GO:0006091~generation of precursor metabolites and energy	7	9,72	8,85E-04

Legend: GO pathway ID - the ID of gene ontologies signaling pathway according to DAVID database; Number of genes in the cascade – the number of genes in the DEG list present in this cascade; % - the percent of genes from the list of FOXA1 target genes, that are present at the pathway; p-value ≤0.05

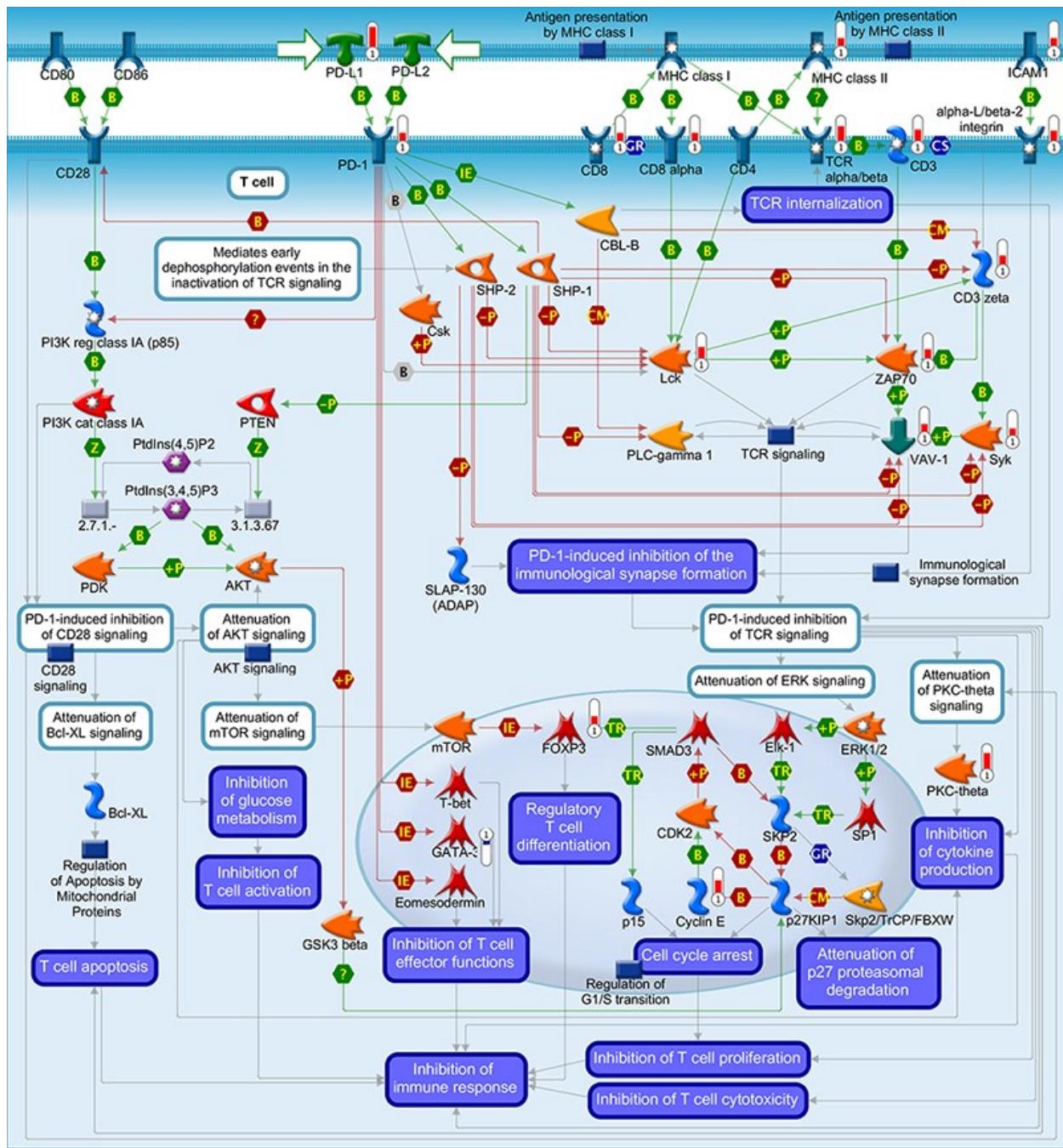
Pathway analysis

Immune component of psoriasis was under extensive investigation in the last decades, and although interferon signaling and leucocyte chemotaxis are not specific for psoriasis, Th1 and Th-17 polarization of T cell population and altered IL-8, IL-17 and IL-23 signaling are currently considered to be “canonic” for psoriasis (21-23). The main sources of cytokines in psoriatic lesion are immune cells, such as dendritic cells and T cells, as well as keratinocytes itself (24). Among the cytokines acting as important regulators of skin homeostasis and inflammation one could mention TNF- α , IFN- γ , IL-1, IL-17, IL-12, IL-21, IL-22, IL-23 (25-27). Keratinocytes don’t express functional receptors to some of them, for example IL-12 and IL-23 (28), thus the influence of such cytokines on the keratinocytes is mediated by other cell types (e.g. Th1, Th17 and Th23). However, a lot of cytokines could directly interact with receptors expressed by keratinocytes and consequently regulate their activation and proliferation, such as IL-1 (IL-1 α and β), IL-2 (IL-4, IL-13, IL-21), IL-4 (IL-4, IL-13), IL-6 (IL-6, OSM, IL-31), IL-10 (IL-19, IL-20, IL-22, IL-24), IL-17 (IL-17A, IL-17C и IL-17F), IFN (IFN- α , IFN- γ), TNF (TNF- α , TNF- β) (27). Pathway analysis had identified the maps “Immune response_IL-17 signaling pathway” and “Immune response: T-cell subsets secreted signals” to be in the top pathways enriched with differentially expressed genes identified by RNA-Seq (Figure 4 and Supplementary Figure 3).

Interleukins are cytokines that play a major role in the development of inflammation. Most of them are not psoriasis-specific and found in other inflammatory disorders. However, the identification of IL-17-producing Th cells, named Th17 cells in 2005 (29) have led to a major breakthrough in the development of anti-psoriatic therapies, and in 2009 IL-17-specific and IL-23p19-specific antibodies showed beneficial effects in trials for psoriasis and comorbidities - ankylosing spondylitis, multiple sclerosis and rheumatoid arthritis, diseases sharing several common mechanisms of aberrant inflammation activation. IL-17A is recently regarded as the key psoriatic cytokine (30-32). This cytokine is extensively produced by Th17 in the site of inflammation and keratinocytes are expressing IL17 receptors constitutively (33), so the cascade is immediately activated, leading to activation of immunity-associated transcription factors and their target genes, coding defensin proteins, S100 proteins, cathelicidin, nitric oxide synthase and different CXCL chemokines mediating neutrophil migration to the site of inflammation (24, 34). The success of target therapy against IL17 or its receptor (antibodies ixekizumab and brodalimumab (35)) confirms its role in the disease. We have identified the vast majority of interleukin genes to be differentially expressed in skin of psoriatic patients (Supp. table 9), and the pathway map “Immune response: T-cell subsets secreted signals” illustrates the main T-cell types responsible for the vas majority of interleukin production in the lesion (Supplementary Figure 3).



Supplementary Figure 3. Immune response: T-cell subsets secreted signals. Illustration generated with MetaCore pathway analysis tool (GeneGO/Thomson Reuters) and enriched with DEGs. Map symbols description could be found in Supp.fig.5. The red bars near gene name illustrate the level of gene overexpression, the blue bars illustrate the level of downregulation of gene expression.. Violet rectangles indicate downstream signaling cascades activated by activation of this pathway.



Supplementary Figure 4. Immune response Inhibitory PD1 signaling in T cells. Illustration generated with MetaCore pathway analysis tool (GeneGO/Thomson Reuters) and enriched with DEGs. Map symbols description could be found in Supp.fig.5. The red bars near gene name illustrate the level of gene overexpression, the blue bars illustrate the level of downregulation of gene expression.. Violet rectangles indicate downstream signaling cascades activated by activation of this pathway.

Regulatory T-cell population (Treg) play an important role in maintenance of homeostasis of T cell populations (36). This type of immune cells is able to protect the organism against autoimmune reactions by several mechanisms of action: expression of T-cell activation/differentiation markers, adhesion molecules, costimulatory molecules and cytotoxic proteins as well as different chemokine receptors (37). Considering the role of acquired immunity and the activity of T effector cells in psoriasis there is a great possibility that altered number or activity of regulatory T-cells plays role in the pathogenesis of this disorder, interfering with skin homeostasis and regulation of immune response (36). Data on Treg prevalence and action in psoriasis is controversial: some researchers report decreased number/activity of this cell type during psoriatic process (38), other point out enhanced number of Treg cells in skin and/or blood of psoriatic patients (39, 40). According to the transcriptomic data obtained, in the analyzed samples of lesional skin of psoriatic patients was observed the enhanced expression of Treg cell markers of (*CD4*, *CD25*, *FOXP3*). This can serve as indirect marker of increased number of Treg cell population in the lesion. The map “Immune response Inhibitory PD-1 signaling in T-cells” (Supplementary Figure 4), illustrating the effector functions of Treg cells on other T cell populations is among the most DEG-enriched pathways.

PD-1 is a cell surface receptor that suppresses the adaptive immune response. Activation of PD-1 signaling by its ligand PD-L1, that was found to be upregulated in psoriasis, inhibits T-cell effector functions: TCR signaling and CD28-mediated co-stimulation, required for T cell activation, proliferation, cytokine production, and cytolytic function. PD-1 signaling also promotes the development of regulatory population T cells, activation Treg master regulator FOXP3 and inhibits the expression of transcription factors that are associated with T cell effector functions (41). However, the abundance of Th17 and Th22 cells in psoriatic lesions suggests an idea of inefficient CD4+CD25+FOXP3+ T-cell function in the course of psoriatic process.

MetaCore™ Quick Reference

User Data

Networks	Maps

Network Objects

Enzymes	
KINASE	PHOSPHATASE
Generic kinase	Generic phosphatase
Protein kinase	Protein phosphatase
Lipid kinase	Lipid phosphatase
PHOSPHOLIPASE	
Generic phospholipase	
PROTEASE	
Generic protease	GTPase
Metalloprotease	G-alpha
	RAS - superfamily
Channels/Transporters	
Generic channel	Receptors
Ligand-gated ion channel	Generic
Voltage-gated ion channel	GPCR
Transporter	Receptors with kinase activity
Groups of Objects	
A complex or a group	Proteins physically connected into a complex or related as a family
Logical association	Determined by logical relations or physical interactions
Custom association	Group of collapsed objects chosen by user

Interactions Between Objects

Effects
Positive / activation
Negative / inhibition
Unspecified

Mechanisms

PHYSICAL INTERACTIONS	
Binding	Compound binds the enzyme or receptor
Cleavage	Cleavage of a protein at a specific site yielding distinctive peptide fragments. Proteolytic cleavage can be carried out by both enzymes and compounds.
Covalent modifications	Protein activity regulation by covalent binding of a small chemical group to the amino acids of an active site.
Phosphorylation	Protein activity is altered via addition of a phosphate group
Dephosphorylation	Protein activity is altered via removal of a phosphate group
Transformation	Protein activity regulation by binding & hydrolysis of GTP
Transport	Transport of a protein or a compound between organelles
Catalysis	Catalysis of an enzymatic reaction
Transcription regulation	Physical binding of a transcription factor to target gene's promoter
MicroRNA binding	Regulation of gene expression by binding of microRNA to target mRNA
FUNCTIONAL INTERACTIONS	
Influence on expression	Compounds change the expression level of target genes indirectly, for instance by binding to upstream receptors
Competition	Protein activity regulation by competition at the substrate binding site
Unspecified interactions	Mechanism is unknown or/and effect is indirect
Drug-Drug interactions, Pharmacological effect	Drugs change pharmacological effects of other drugs, for instance by competing for common metabolizing enzymes or organic transporters
Drug-Drug interactions, Toxic effect	Drugs change toxic effects of other drugs, for instance by competing for drug metabolism enzymes or organic transporters
LOGICAL RELATIONS	
Group relation	Object belongs to a generic group of related objects
Complex subunit	Protein is a subunit of a protein complex
Similarity relation	Chemically similar compounds with chosen Tanimoto similarity score

Links on Networks

- Incoming interaction When the mouse is over object, yellow link indicates direction to object
- Outgoing interaction Cyan link indicates direction from the object

Interactions from custom list (MetaLink™)

- Interaction is in the network Interaction is represented by a thin solid line and is highlighted in blue
- Interaction is in the base, but not in network Interaction is highlighted in yellow
- Interaction is in the network Interaction is highlighted in magenta

Canonical pathways

- Canonical pathway The link is highlighted in a thick cyan or magenta line

Links on Maps

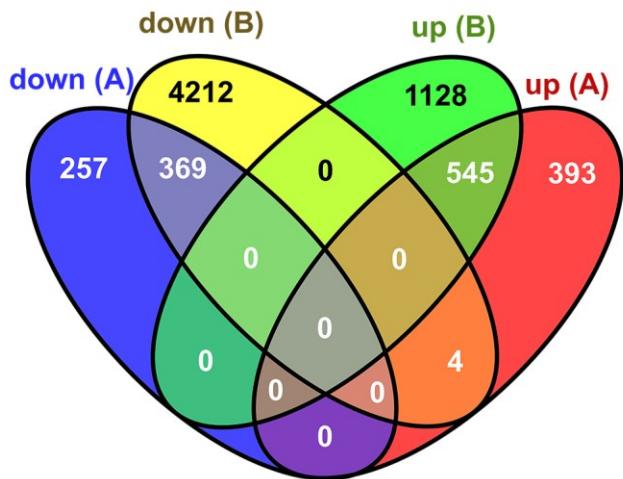
- Disrupts in disease
- Weakens in disease
- Emerges in disease
- Enhances in disease
- Species specific interactions

Objects on Maps

Localization	Other Map Objects
	Mitochondria
	EPR
	Golgi
	Nucleus
	Lysosome
	Peroxisome
	Cytoplasm
	Extracellular
	Note
	Normal process
	Pathological process
	Normal map
	Disease map
	Species specific object
	Path start

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Supplementary Figure 5. Legend for the MetaCore pathway maps.



Supplementary Figure 6. Comparison of the DEG lists ($\text{FC}>1.5$, $\text{FDR}<0.05$) identified in this study (A) and in the analysis of Li. et al (B). up – upregulated differentially expressed genes, down – downregulated genes.

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